



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 147987

To: Sarvamangala Devi
Location: REM 3C18
Art Unit: 1645
Wednesday, March 16, 2005

Case Serial Number: 10/041775

From: Beverly Shears
Location: Remsen Bldg.
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Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



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Scoring table:	BLOSUM62					
Gapop:	10.0 , Gapext: 0.5					
Searched:	1612378 seqs, 512079187 residues					
Total number of hits satisfying chosen parameters:	1612378					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing First 45 summaries					
Database :	UniProt_03;* 1: uniprot_sprot;* 2: uniprot_trembl;*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES	\$					
Result No.	Score	Query	Match	Length	DB ID	Description
1	95.0	93.5	689	2	Q53599	Q53599 staphylococ
2	95.0	93.5	689	2	Q9z4P5	Q9z4P5 staphylococ
3	95.0	93.5	689	2	Q6FBF8	Q6FBF8 staphylococ
4	90.7	89.3	584	2	Q9xAS5	Q9xAS5 staphylococ
5	88.8	87.5	687	2	Q9z2Z4	Q9z2Z4 staphylococ
6	88.6	87.5	657	2	Q07318	Q07318 staphylococ
7	88.4	87.1	476	2	Q99QS1	Q99QS1 staphylococ
8	88.1	86.8	581	2	QBvYR4	QBvYR4 staphylococ
9	814.5	80.2	584	2	Q9k4S8	Q9k4S8 staphylococ
10	80.1	78.9	535	2	Q9zJ2	Q9zJ2 staphylococ
11	31.8	31.3	121	1	OMP7_STAUU	P21223 staphylococ
12	21.0	20.7	144	2	Q8DQE3	Q8nxe3 staphylococ
13	21.0	20.7	144	2	Q99VA9	Q99VA9 staphylococ
14	21.0	20.7	144	2	Q7A6G0	Q7a6G0 staphylococ
15	21.0	20.7	144	2	Q6GAU5	Q6gaus staphylococ
16	21.0	20.7	144	2	Q6GIA6	Q6gia6 staphylococ
17	146.5	14.4	141	2	Q8S961	Q8g961 staphylococ
18	146.5	14.4	141	2	Q99S64	Q99s64 staphylococ
19	146.5	14.4	141	2	Q7AO90	Q7ao90 staphylococ
20	146.5	14.4	141	2	Q7A483	Q7a483 staphylococ
21	146.5	14.4	141	2	Q6G7B0	Q6g7b0 staphylococ
22	144.5	14.2	141	2	Q6GEM4	Q6gem4 staphylococ
23	136	13.4	106	2	Q99QS2	Q99qs2 staphylococ
24	135	13.3	96	2	Q8NVR5	Q8nvr5 staphylococ
25	118	11.6	1178	2	Q78BM0	Q78bm0 fusobacteri
26	118	11.6	1620	2	Q8JIV3	Q8jiv3 plasmoidium
27	116	11.4	1792	2	Q8DD94	Q8id94 plasmoidium
28	115	11.3	374	2	Q8DQE1	Q8dqe1 streptococc
29	114.5	11.3	640	1	GYRB_SPIC1	P34031 spiroplasma
30	114.5	11.3	1272	2	Q9PR01	Q9pr01 ureaplasma
31	11.1	1016	2	Q7DPD5	Q7dpd5 plasmoidium	

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.	Qy 4 SHHHHHHGSQLIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 63
NCBI_TaxID=1280;	41 SLHGGYSKIQIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 100
RP . SEQUENCE FROM N.A.	
RC STRAIN=Newman; Heilmann M.; Heilmann C.; Peters G.;	Qy 64 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 123
RA Hussain S.M.; Hussain S.M., Heilmann M., Heilmann C., Peters G.;	Db 101 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 160
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AJ121841; CAA10802; 1; -.	Qy 124 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 183
DR Int'Pro; IPR005298; MAP; 6.	Db 161 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 220
PF Pfam; PF03642; MAP; 6.	
KW SIGNAL; 1 30 Potential.	
FT CHAIN 31 689 AA; 76860 MW; CF88802B4F47C9CD CRC64;	Qy 184 NFKNGTKKVVDLKGAGY 200
SQ SEQUENCE 689 AA; 76860 MW; CF88802B4F47C9CD CRC64;	Db 221 NFKNGTKKVVDLKGAGY 237
Query Match Score 95%; DB 2; Length 689;	RESULT 4
Best Local Similarity 97.0%; Pred. No. 1e-55; Indels 0; Gaps 0;	Q9XAS5 PRELIMINARY; PRT; 584 AA.
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	ID Q9XAS5; AC Q9XAS5;
Qy 4 SHHHHHHGSQLIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 63	DT 01-NOV-1999 (TREMBLrel. 12, Created)
Db 41 SLHGGYSKIQIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 100	DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
Qy 64 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 123	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db 101 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 160	DB Map-7 protein precursor.
Qy 124 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 183	OS Name-map-/;
Db 161 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 220	Staphylococcus aureus.
Qy 184 NFKNGTKKVVDLKGAGY 200	OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
Db 221 NFKNGTKKVVDLKGAGY 237	OX NCBI_TaxID=1280;
Query Match Score 95%; DB 2; Length 689;	RP SEQUENCE FROM N.A.
Best Local Similarity 97.0%; Pred. No. 1e-55; Indels 0; Gaps 0;	RA Hussain Shaikh M.; Heilmann C.; Peters G.; Herrman M.;
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
Qy 4 SHHHHHHGSQLIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 63	[1]
Db 41 SLHGGYSKIQIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 100	DR IPI2005298; MAP; 5.
Qy 64 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 123	DR Pfam; PF03642; MAP; 5.
Db 101 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 160	KW Signal.
Qy 124 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 183	FT SIGNAL 1 30 Potential.
Db 161 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 220	FT CHAIN 31 584 AA; 65173 MW; OA9383C5F639C1 CRC64;
Qy 184 NFKNGTKKVVDLKGAGY 200	SEQUENCE 584 AA;
Db 221 NFKNGTKKVVDLKGAGY 237	DB 89 3%; DR 907; DB 2; Length 584;
Query Match Score 95%; DB 2; Length 689;	Best Local Similarity 93 4%; Pred. No. 6.5e-53;
Best Local Similarity 97.0%; Pred. No. 1e-55; Indels 0; Gaps 0;	Matches 184; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	Qy 4 SHHHHHHGSQLIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 63
Q6GFBB 06GFBB PRELIMINARY; PRT; 689 AA.	41 SLHGGYSKIQIPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 100
AC Q6GFBB; DT 05-JUL-2004 (TREMBLrel. 27, Created)	Qy 64 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 123
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	Db 101 RLSKQAKYTTHFKNGTKRVDLKGHTADLINTSDIKASVNVTDTKQVQDKEAKANVQ 160
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	Qy 124 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 183
MHC class II analysis.	Db 161 VPYTTVNGTSONISSLTFKNNQISYKDIEENKVKSVLVFNRGKSDIDL 220
OrderdLocusNames=SAR2030;	
OS Staphylococcus aureus (strain MRSA52).	Qy 184 NFKNGTKKVVDLKGAGY 200
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.	Db 221 NFKNGTKKVVDLKGAGY 237
OX NCBI_TaxID=282458;	
RN [1]	RESULT 5
RP SUBMED-15213324; DOI=10.1073/pnas.0402521101;	Q9S2Z4 PRELIMINARY; PRT; 687 AA.
RA Holden M.T.G., Peil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,	ID Q9S2Z4
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin Barron A.,	AC Q9S2Z4
RA Basow N., Bentley S.D., Chillingworth C., Chillingworth T.,	DT 01-MAY-2000 (TREMBLrel. 13, Created)
RA Churcher C., Clark L., Corron C., Cronin A., Doggett J., Dowd L.,	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Munqali K.,	DE Cell surface protein map-w precursor.
RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,	GN Name-map-w;
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,	OS Staphylococcus aureus. Bacteria; Firmicutes; Bacillales; Staphylococcus.
RA Spratt B.G., Parkhill J.,	
RT "Complete genomes of two clinical Staphylococcus aureus strains:	
RT evidence for the rapid evolution of virulence and drug resistance."	
RL proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).	
DR EMBL; BX571856; CAG41016.1; -.	
DR InterPro; IPR005298; MAP; 6.	
DR Pfam; PF03642; MAP; 6.	
KW Complete Proteome.	
SQ SEQUENCE 689 AA; 76848 MW; 4141D8900549099D CRC64;	
Query Match Score 95%; DB 2; Length 689;	
Best Local Similarity 97.0%; Pred. No. 1e-55; Indels 0; Gaps 0;	
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	

OX NCBI_TaxID=1280;							
RN [1]	SEQUENCE FROM N.A.						
RP							
RC STRAIN=Swood 46;							
RA Hussain Shaikh M., Heilmann C., Peters G., Herrmann M., Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.							
RL DRB439; CAB51807.1; -.							
DR InterPro: IPR00598; MAP.							
DR Pfam: PF03642; MAP; 6.							
RW SIGNAL							
FT SIGNAL	1	30	Potential.				
SC SEQUENCE	687 AA;	77072 MW;	91D42532DB7DD2B CRC64;				
Best Local Similarity	91.3%	Score 888.5;	DB 2;	Length 687;			
Matches	178;	Conservative	7;	Mismatches 9;	Indels 1;	Gaps 1;	
Qy 6 HHHHHGSQLQIPTYTIVNGTSQNLISSLTFNKNQISYKDIEENKVSKVLYFNRGISDIDRL 65							
Db 43 HHGHSNTQIPTYTIVNGTSQNLISSLTFNKNQISYKDIEENKVSKVLYFNRGISDIDRL 102							
Qy 66 SKQAKTYTHFKNGTKRVDLKAGIHTADLINTSDIKAISSVNDTKKQDKEAKANVQV 125							
Db 103 SKQAEYTHFKNGTKRVDLKGSYITADLINTSDIKAISSVNDTKKQDK-AKANVQV 161							
Qy 126 YTITVNGTSQNLISSLTFKKNQISYKDIEENNVKSKVLYFNRGIDTDVLRLSKQAKFTVNF 185							
Db 162 YTITVNGTSQNLISSLTFKKNQISYKDIEENNVKSKVLYFNRGIDTDVLRLSKQAKFTVNF 221							
Qy 186 KNGTKVVDLKGAYI 200							
Db 222 KNGTKVVDLKGAYI 236							
RESUME 6							
ID 007318 PRELIMINARY; PRT; 657 AA.							
AC 007318							
DT 01-JUL-1997 (TREMBLrel. 04; Created)							
DT 01-JUL-1997 (TREMBLrel. 04; Last sequence update)							
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)							
RL Outer surface binding 70kD protein (Fragment).							
OS Staphylococcus aureus.							
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.							
OX NCBI_TaxID=1280;							
RN SEQUENCE FROM N.A.							
RP STRAIN=W 46;							
RA Youself Y.; Draeger R.; Schiltz M.; Peter H.; Schlesier M.; Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.							
RL InterPro: IPR00598; MAP.							
DR Pfam: PF03642; MAP; 6.							
FT NON_TER 1	1	PRED 1					
SC SEQUENCE	657 AA;	74044 MW;	1A7980DF1B7E09A3 CRC64;				
Query Match	87.3%;	Score 886.5;	DB 2;	Length 657;			
Best Local Similarity	90.8%;	Pred. No. 1.0e-5+;					
Matches	177;	Conservative	8;	Mismatches 9;	Indels 1;	Gaps 1;	
Qy 6 HHHHHGSQLQIPTYTIVNGTSQNLISSLTFNKNQISYKDIEENKVSKVLYFNRGISDIDRL 65							
Db 13 HHGHSNTQIPTYTIVNGTSQNLISSLTFNKNQISYKDIEENKVSKVLYFNRGISDIDRL 72							
Qy 66 SKQAKTYTHFKNGTKRVDLKAGIHTADLINTSDIKAISSVNDTKKQDKEAKANVQV 125							
Db 73 SKQAEYTHFKNGTKRVDLKGSYITADLINTSDIKAISSVNDTKKQDK-AGANVQV 131							
Qy 126 YTITVNGTSQNLISSLTFKKNQISYKDIEENNVKSKVLYFNRGIDTDVLRLSKQAKFTVNF 185							
Db 132 YTITVNGTSQNLISSLTFKKNQISYKDLEDVKSYLSENRGIDTDVLRLSKQAKFTVNF 191							
Qy 186 KNGTKVVDLKGAYI 200							
Db 222 KNGTKVVDLKGAYI 236							
RESULT 8							
ID Q8NVR4 PRELIMINARY; PRT; 581 AA.							
AC Q8NVR4;							
DT 01-OCT-2002 (TREMBLrel. 22; Created)							
DT 01-OCT-2002 (TREMBLrel. 22; Last sequence update)							
DT 01-Mar-2004 (TREMBLrel. 26; Last annotation update)							
DE Truncated cell surface protein map.w.							
GN Name=truncated map-W; OrderedLocusNames=MW1880;							
OS Staphylococcus aureus (strain MW2);							
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.							
OX NCBI_TaxID=196620;							
RN SEQUENCE FROM N.A.							
RC STRAIN=MW2;							
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;							

RA	Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Naga I., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,	QY	64 RLSKQAKYVHFNGTKRVDLKGAGIHTADLINTSDIKAIISVNVDTKQVKDKEA-KANV 122
RA	Yamamoto K., Hiramatsu K., "Genome and virulence determinants of high virulence community-acquired MRSA.", Lancet 359;1819-1827 (2002).	Db	101 RLSKQAKYVHFNGTKRVDLKGAGIHTADLINTSEIKAININVDTKQVEDDKKKDQANY 160
RT		QY	123 QVPXTITYNTGTSQNLSSLTENKQOISYKDLENNTKSVLKSNRGTTDYLRSKQAKFT 182
RT		Db	161 QVPXTITYNTGTSQNLSSLTENQNQNISYKDLEDKVSLESNRGTTDYLRSKQAKFT 220
RL			
DR	InterPro; IPR05298; MAP.		
DR	Pfam; PF01642; MAP; 5.		
KW	Complete proteome; SEQUENCE 581 AA;	QY	183 VNFKNGTKRVIDLKSGIY 200
SQ	SEQUENCE 581 AA; 65095 MW; 912F70CDCD8BBC68 CRC64;	Db	221 VNFKNGTKRVIDLKSGIY 238
Query Match	Best Local Similarity 86.8%; Score 881.5%; DB 2; Length 581; Matches 176; Conservative 6; Mismatches 10; Indels 1; Gaps 1;	RESULT 10	Q9Z4U2 PRELIMINARY; PRT; 535 AA.
Qy	6 HHHAHGSQIPQTITYNTGTSQNLSSLTENKQOISYKDLENNTKSVLKSNRGTTDYLRSKQAKFT 65	AC	Q9Z4U2; PRELIMINARY;
Db	43 HHGHNSNTQIPQTITYNTGTSQNLSSLTENKQOISYKDLENNTKSVLKSNRGTTDYLRSKQAKFT 102	AC	Q9Z4U2; PRELIMINARY;
Qy	66 SKQAKYVHFNGTKRVDLKGAGIHTADLINTSDIKAIISVNVDTKQVKDKEA-KANVOP 125	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
Db	103 SKQAEYTTHFKNGTKKVIDLKSGIYTADLINTSDIKAIISVNVDTKQPKDK-AKANVOP 161	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
Qy	126 YTITVNTGTSQNLSSLTENKQOISYKDLENNTKSVLKSNRGTTDYLRSKQAKFTVNF 185	DE	Map Protein (Fragment).
Db	162 YTITVNTGTSQNLSSLTENKQOISYKDLENNTKSVLKSNRGTTDYLRSKQAKFTVNF 221	GN	Name=map;
Qy	186 KNGTKVKVIDLKSGIY 200	OS	Staphylococcus aureus.
Db	222 KNGTKVKVIDLKSGIY 236	OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
		OX	NCBI_TaxID=1280; RN [1];
		RN	SEQUENCE FROM N.A.
		RP	SEQUENCE FROM N.A.
		RC	STRAIN=Newman; McDevitt D., Kapur V., Hook M.;
		RA	Kreikemeyer B., McDevitt D., Kapur V., Hook M.;
		RL	Submitted (PEB-1998) to the EMBL/GenBank/DDBJ databases.
		EMBL; AJ22806; CAI1155.1; -.	
		DR	InterPro; IPR05298; MAF.
		DR	Pfam; PF03642; MAP; 5.
		NON_TER	NON_TER 1 1 Map protein.
		FT	FT CHAIN 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
		SQ	SEQUENCE 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
RESULT 9		Query Match	78.9%; Score 801.5%; DB 2; Length 535;
Q9K4SB	PRELIMINARY; PRT; 584 AA.	Best Local Similarity	84.6%; Pred. No. 7.1e-46;
AC	Q9K4SB; PRELIMINARY; PRT; 584 AA.	Matches 159; Conservative 19; Mismatches 9; Indels 1; Gaps 1;	
ID		DR	InterPro; IPR05298; MAF.
Q9K4SB		DR	Pfam; PF03642; MAP; 5.
AC		NON_TER	NON_TER 1 1 Map protein.
Q9K4SB		FT	FT CHAIN 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
AC		SQ	SEQUENCE 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
RESULT 9		Query Match	78.9%; Score 801.5%; DB 2; Length 535;
Q9K4SB	PRELIMINARY; PRT; 584 AA.	Best Local Similarity	84.6%; Pred. No. 7.1e-46;
AC	Q9K4SB; PRELIMINARY; PRT; 584 AA.	Matches 159; Conservative 19; Mismatches 9; Indels 1; Gaps 1;	
ID		DR	InterPro; IPR05298; MAF.
Q9K4SB		NON_TER	NON_TER 1 1 Map protein.
AC		FT	FT CHAIN 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
Q9K4SB		SQ	SEQUENCE 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
RESULT 9		Query Match	78.9%; Score 801.5%; DB 2; Length 535;
Q9K4SB	PRELIMINARY; PRT; 584 AA.	Best Local Similarity	84.6%; Pred. No. 7.1e-46;
AC	Q9K4SB; PRELIMINARY; PRT; 584 AA.	Matches 159; Conservative 19; Mismatches 9; Indels 1; Gaps 1;	
ID		DR	InterPro; IPR05298; MAF.
Q9K4SB		NON_TER	NON_TER 1 1 Map protein.
AC		FT	FT CHAIN 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
Q9K4SB		SQ	SEQUENCE 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
RESULT 9		Query Match	78.9%; Score 801.5%; DB 2; Length 535;
Q9K4SB	PRELIMINARY; PRT; 584 AA.	Best Local Similarity	84.6%; Pred. No. 7.1e-46;
AC	Q9K4SB; PRELIMINARY; PRT; 584 AA.	Matches 159; Conservative 19; Mismatches 9; Indels 1; Gaps 1;	
ID		DR	InterPro; IPR05298; MAF.
Q9K4SB		NON_TER	NON_TER 1 1 Map protein.
AC		FT	FT CHAIN 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
Q9K4SB		SQ	SEQUENCE 535 AA; 60459 MW; D566318AC64F2A1 CRC64;
RESULT 9		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
Q9K4SB	Best Local Similarity 81.8%; Pred. No. 1e-46;	Best Local Similarity	81.8%; Pred. No. 1e-46;
AC	Q9K4SB; Best Local Similarity 81.8%; Pred. No. 1e-46;	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
ID		DR	InterPro; IPR05298; MAF.
Q9K4SB		NON_TER	NON_TER 1 1 Map protein.
AC		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
Q9K4SB		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
RESULT 11		Query Match	80.2%; Score 814.5%; DB 2; Length 584;
OMP7_STAAU	STANDARD; PRT; 121 AA.	Best Local Similarity	81.8%; Pred. No. 1e-46;
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;	
OMP7_STAAU		DR	InterPro; IPR05298; MAF.
OMP7_STAAU		NON_TER	NON_TER 1 1 Map protein.
OMP7_STAAU		FT	FT CHAIN 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;
OMP7_STAAU		SQ	SEQUENCE 584 AA; 65

DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)	Query Match Score 210; DB 2; Length 144;
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)	Best Local Similarity 44.3%; Pred. No. 8.1e-07; Mismatches 32; Indels 0; Gaps 0;
DE	SA0841	protein.	Matches 45; Conservative 22; Mis
GN	OrderedLocusName=SA0841;	Y	14 IPYTIVNGTQNQLSSLTENKNOQISYKDIEINKVSKVLYFNRGSDIDDLRLSKQAKYTV 73
OS	Staphylococcus aureus (strain N315).	Db	48 VPYTIAVDGIMAFNQSYLNLPKDSQSYLNLFDNSIKOIDINVTK 107
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.	Qy	74 HFKNGTKRVIDLKAGIHTADLINTSDIKAISVNVTK 110
OX	NCBI_TaxID=158879;	Db	108 TWKDGSKEVDLKKDSYTNLFDNSIKOIDINVTK 110
RN	SEQUENCE FROM N.A.	[1]	
RX	MEDLINEID=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;		
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuraka H., Kobayashi I.,		
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,		
RA	Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,		
RA	Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaijo C.,		
RA	Sekimoto K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,		
RA	Kaneko M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,		
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,		
RT	"Whole genome sequencing of meticillin-resistant Staphylococcus aureus";		
RL	Lancet 357:1225-1240(2001).		
DR	EMBL; AP001322; BAB43081..1; -.		
DR	InterPro; IPR005298; MAP.		
DR	Pfam; PF03642; MAP; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 144 AA; 15898 MW; ABFE3FE30ED9506C CRC64;		
RN	SEQUENCE FROM N.A.	[1]	
RX	PubMed=15213344; DOI=10.1073/pnas.0402521101;		
RA	Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,		
RA	Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,		
RA	Bason N., Bentley S.D., Chillingworth T., Feltwell T., Hance Z., Harris C., Corbin C., Clark L., Corton A., Doggett J., Dowd L.,		
RA	Churcher C., Clark L., Corton A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris C., Hauser H., Holroyd S., Jagels K., James K.D., Leonard N., Line A., Mayes R., Moulis S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch B., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.,		
RA	"Complete genomes of two clinical Staphylococcus aureus strains evidence for the rapid evolution of virulence and drug resistance.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).		
DR	InterPro; IPR005298; MAP.		
DR	PF03642; MAP; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 144 AA; 15868 MW; A29B2AE30ED9456C CRC64;		
RN	SEQUENCE FROM N.A.	[1]	
RX	PubMed=15213324; DOI=10.1073/pnas.0402521101;		
RA	Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,		
RA	Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,		
RA	Bason N., Bentley S.D., Chillingworth T., Feltwell T., Hance Z., Harris C., Corbin C., Clark L., Corton A., Doggett J., Dowd L.,		
RA	Churcher C., Clark L., Corton A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris C., Hauser H., Holroyd S., Jagels K., James K.D., Leonard N., Line A., Mayes R., Moulis S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch B., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.,		
RA	"Complete genomes of two clinical Staphylococcus aureus strains evidence for the rapid evolution of virulence and drug resistance.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).		
DR	InterPro; IPR005298; MAP.		
DR	PF03642; MAP; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 144 AA; 15838 MW; F29A2AE30EDCD4563 CRC64;		

RX	MBDLINE5=222215721; PubMed=12228315;			
RX	DOI=10.1128/IAI.70.10.5835-5845.2002;			
RA	Yamaguchi T., Nishifujii K., Sabaki M., Fudaba Y., Aepfelbacher M.,			
RA	Ohara M., Komatsu H., Amagai M.; Sugai M.;			
RT	"Identification of the Staphylococcus aureus end-pathogenicity island which encodes a novel exfoliative toxin, ETX, and EDIN-B";			
RT	Infect Immun. 70:5835-5845(2002).			
RL	EMBL: AB057421; EAC222949.1; -.			
DR	InterPro: IPR00598; MAP.			
DR	Fram; PF03642; MAP; 1.			
KW	Hypothetical protein.			
SEQUENCE	141 AA; 15455 MW; 420C9AE720E8DE51 CRC64;			
SQ	Q99S64 PRELIMINARY; PRT; 141 AA.			
Query Match	14.4%; Score 146.5; DB 2; Length 141;			
Best Local Similarity	31.8%; Pred. No. 0.014;			
Matches	34; Conservative 26; Mismatches 40; Indels 7; Gaps 1;			
Qy	1 MRGSHHHHHGGSQIPYTITVNTGSQNLISSLTPNQKQISYKDIEENKVSKVLYFNGRISD 60			
Db	41 MDGKH-----TVPTITSVDGITALHRTYFVPPENKVKLYQEIDSKVTKNELASQRTTT 93			
Qy	61 IDLRLSKOAKTIVTHFKNGTKRVVDLKAGIHTADLINTSDIKAISSVNV 107			
Db	94 EKINNAQTATYLTTLNDGKCKVNLKNDDKNSIDPSTIKIQIVV 140			
RESULT 18				
Q99S64	PRELIMINARY; PRT; 141 AA.			
AC	Q99S64; 17; Created)			
DT	01-JUN-2001 (TREMBLrel. 17; Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17; Last annotation update)			
DT	01-MAR-2004 (TREMBLrel. 26; Last annotation update)			
DE	Hypothetical protein.			
GN	OrderedLocusName=SAV2205;			
Staphylococcus aureus (strain Mu50 / ATCC 700699).				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcaceae.			
NCBI_TaxID=158878;				
RN	SEQUENCE FROM N.A.			
RC	STRAIN=Mu50 / ATCC 700699;			
RX	MBDLINE5=21311952; PubMed=11418146; DOI=10.11016/S0140-6736(00)04403-2;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi T.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,			
RA	Kanamori M., Matsunaga H., Maruyama A., Murakami H., Hosoyama A.,			
RA	Mizutani-Uji Y., Takashita N., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,			
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,			
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,			
RT	"Whole genome sequencing of meticillin-resistant Staphylococcus aureus";			
RL	357.1225-1240(2001).			
DR	BMBL; AP003364; BAB53367.1; -.			
DR	PIR: H90016; H90016.			
DR	InterPro; IPR005298; MAP.			
PFam	PF03642; MAP; 1.			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 141 AA; 15426 MW; 42142DB720E8DE51 CRC64;			
Query Match	14.4%; Score 146.5; DB 2; Length 141;			
Best Local Similarity	31.8%; Pred. No. 0.014;			
Matches	34; Conservative 26; Mismatches 40; Indels 7; Gaps 1;			
Qy	1 MRGSHHHHHGGSQIPYTITVNTGSQNLISSLTPNQKQISYKDIEENKVSKVLYFNGRISD 60			
Db	41 MDGKH-----TVPTITSVDGITALHRTYFVPPENKVKLYQEIDSKVTKNELASQRTTT 93			
Qy	61 IDLRLSKOAKTIVTHFKNGTKRVVDLKAGIHTADLINTSDIKAISSVNV 107			
Db	94 EKINNAQTATYLTTLNDGKCKVNLKNDDKNSIDPSTIKIQIVV 140			
RESULT 20				
Q99S64	PRELIMINARY; PRT; 141 AA.			
AC	Q99S64; 17; Created)			
DT	01-JUN-2001 (TREMBLrel. 17; Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17; Last annotation update)			
DT	01-MAR-2004 (TREMBLrel. 26; Last annotation update)			
DE	Hypothetical protein.			
GN	OrderedLocusName=SAV2205;			
Staphylococcus aureus (strain Mu50 / ATCC 700699).				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcaceae.			
NCBI_TaxID=158878;				
RN	SEQUENCE FROM N.A.			
RC	STRAIN=Mu50 / ATCC 700699;			
RX	MBDLINE5=21311952; PubMed=11418146; DOI=10.11016/S0140-6736(00)04403-2;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi T.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,			
RA	Kanamori M., Matsunaga H., Maruyama A., Murakami H., Hosoyama A.,			
RA	Mizutani-Uji Y., Takashita N., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,			
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,			
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,			
RT	"Whole genome sequencing of meticillin-resistant Staphylococcus aureus";			
RL	357.1225-1240(2001).			
DR	BMBL; AP003364; BAB53367.1; -.			
DR	PIR: H90016; H90016.			
DR	InterPro; IPR005298; MAP.			
PFam	PF03642; MAP; 1.			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 141 AA; 15426 MW; 42142DB720E8DE51 CRC64;			
Query Match	14.4%; Score 146.5; DB 2; Length 141;			
Best Local Similarity	31.8%; Pred. No. 0.014;			
Matches	34; Conservative 26; Mismatches 40; Indels 7; Gaps 1;			
Qy	1 MRGSHHHHHGGSQIPYTITVNTGSQNLISSLTPNQKQISYKDIEENKVSKVLYFNGRISD 60			
Db	41 MDGKH-----TVPTITSVDGITALHRTYFVPPENKVKLYQEIDSKVTKNELASQRTTT 93			
Qy	61 IDLRLSKOAKTIVTHFKNGTKRVVDLKAGIHTADLINTSDIKAISSVNV 107			
Db	94 EKINNAQTATYLTTLNDGKCKVNLKNDDKNSIDPSTIKIQIVV 140			
RESULT 19				

Qy	1	MRGSHHHHHGSQLIPTTYGTNTQNLISSLTENKVKSYDKINQISYDKEIDNKVKSYLYFNRGISD 60 AC : : : : : : : : : : : : : : : : : : : : : : : : DB 41 MDGKH----TVPTISVUDGITALHRTYFVFPENKKVLYQEIDSKVKNELASORGVTT 93	SEQUENCE FROM N.A. PubMed=15213324; DOI=10.1073/pnas.0402521101; Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Churcher C., Chillingworth T., Clark L., Corlett C., Cronin A., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jigels K., James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance." proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004). RN [1] _TaxID=282459;	RESULT 21 Q6G7B0 PRELIMINARY; PRT; 141 AA. ID Q6G7B0; AC ; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DB Putative exported protein. OrderedLocusName=SAS2104; Staphylococcus aureus (strain MSSA476). Bacteria; Firmicutes; Bacillales; Staphylococcaceae. NCBI_TaxID=282459;	Query Match Best Local Similarity 14.4%; Score 146.5; DB 2; Length 141; Matches 34; Conservative 26; Mismatches 40; Indels 7; Gaps 1; Sequence 141 AA; 15426 MW; 42142DB720E8DE51 CRC64;	DR InterPro; IPR005298; MAP.; DR InparPro; IPR005298; MAP.; DR Pfam; PF03642; MAP.; DR Complete proteome.
Qy	61 IDLRLSKQAKTYPFKNGTKRVDLKAGIHTADLINTSDIKAI SVN 107 AC : : : : : : : : : : : : : : : : : : DB 94 EKINNAQTATYTLTLDNGKVKVNLLKNDAKNSIDPSTIKOIQIVV 140	SEQUENCE FROM N.A. PubMed=15213324; DOI=10.1073/pnas.0402521101; Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Churcher C., Chillingworth T., Clark L., Corlett C., Cronin A., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jigels K., James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance." proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004). RN [1] _TaxID=282459;	RESULT 22 Q6GEM4 PRELIMINARY; PRT; 141 AA. ID Q6GEM4; AC ; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DB Putative exported protein. OrderedLocusName=SAR2295; Staphylococcus aureus (strain MRSA252). Bacteria; Firmicutes; Bacillales; Staphylococcaceae. NCBI_TaxID=282458;	Query Match Best Local Similarity 14.4%; Score 136; DB 2; Length 106; Matches 26; Conservative 27; Mismatches 43; Indels 0; Gaps 0; Sequence 106 AA; 12260 MW; 605482EDD4CC2200 CRC64;	DR InterPro; IPR005298; MAP.; DR Pfam; PF03642; MAP.; DR Complete proteome.	
Qy	61 IDLRLSKQAKTYPFKNGTKRVDLKAGIHTADLINTSDIKAI SVN 107 AC : : : : : : : : : : : : : : : : DB 94 EKINNAQTATYTLTLDNGKVKVNLLKNDAKNSIDPSTIKOIQIVV 140	SEQUENCE FROM N.A. PubMed=15213324; DOI=10.1073/pnas.0402521101; Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Churcher C., Chillingworth T., Clark L., Corlett C., Cronin A., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jigels K., James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance." proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004). RN [1] _TaxID=282459;	RESULT 22 Q6GEM4 PRELIMINARY; PRT; 141 AA. ID Q6GEM4; AC ; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DB Putative exported protein. OrderedLocusName=SAR2295; Staphylococcus aureus (strain MRSA252). Bacteria; Firmicutes; Bacillales; Staphylococcaceae. NCBI_TaxID=282458;	Query Match Best Local Similarity 13.4%; Score 136; DB 2; Length 106; Matches 26; Conservative 27; Mismatches 43; Indels 0; Gaps 0; Sequence 106 AA; 12260 MW; 605482EDD4CC2200 CRC64;	DR InterPro; IPR005298; MAP.; DR Pfam; PF03642; MAP.; DR Complete proteome.	
Qy	61 IDLRLSKQAKTYPFKNGTKRVDLKAGIHTADLINTSDIKAI SVN 107 AC : : : : : : : : : : : : : : : : DB 94 EKINNAQTATYTLTLDNGKVKVNLLKNDAKNSIDPSTIKOIQIVV 140	SEQUENCE FROM N.A. PubMed=15213324; DOI=10.1073/pnas.0402521101; Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Churcher C., Chillingworth T., Clark L., Corlett C., Cronin A., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jigels K., James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance." proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004). RN [1] _TaxID=282459;	RESULT 22 Q6GEM4 PRELIMINARY; PRT; 141 AA. ID Q6GEM4; AC ; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DB Putative exported protein. OrderedLocusName=SAR2295; Staphylococcus aureus (strain MRSA252). Bacteria; Firmicutes; Bacillales; Staphylococcaceae. NCBI_TaxID=282458;	Query Match Best Local Similarity 13.4%; Score 136; DB 2; Length 106; Matches 26; Conservative 27; Mismatches 43; Indels 0; Gaps 0; Sequence 106 AA; 12260 MW; 605482EDD4CC2200 CRC64;	DR InterPro; IPR005298; MAP.; DR Pfam; PF03642; MAP.; DR Complete proteome.	
Qy	61 IDLRLSKQAKTYPFKNGTKRVDLKAGIHTADLINTSDIKAI SVN 107 AC : : : : : : : : : : : : : : : : DB 94 EKINNAQTATYTLTLDNGKVKVNLLKNDAKNSIDPSTIKOIQIVV 140	SEQUENCE FROM N.A. PubMed=15213324; DOI=10.1073/pnas.0402521101; Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Churcher C., Chillingworth T., Clark L., Corlett C., Cronin A., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jigels K., James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J., Whitehead S., Barrell B.G., "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance." proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004). RN [1] _TaxID=282459;	RESULT 22 Q6GEM4 PRELIMINARY; PRT; 141 AA. ID Q6GEM4; AC ; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DB Putative exported protein. OrderedLocusName=SAR2295; Staphylococcus aureus (strain MRSA252). Bacteria; Firmicutes; Bacillales; Staphylococcaceae. NCBI_TaxID=282458;	Query Match Best Local Similarity 13.4%; Score 136; DB 2; Length 106; Matches 26; Conservative 27; Mismatches 43; Indels 0; Gaps 0; Sequence 106 AA; 12260 MW; 605482EDD4CC2200 CRC64;	DR InterPro; IPR005298; MAP.; DR Pfam; PF03642; MAP.; DR Complete proteome.	

RT	parasite Plasmidium yoelii.
Nature	419:512-519 (2002).
- - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	
CC	DR
CC	DR IntePro; IPR03900; KID_repeat.
CC	DR Pfam; PF02524; KID_9.
KW	Hypothetical protein.
SO	SEQUENCE 2341 AA; 266712 MW; 51D2041A084F4BAS CRC64;
Query Match	11.1%; Score 112.5; DB 2; Length 2341;
Best Local Similarity	27.0%; Pred. No. 69;
Matches 54; Conservative 37; Mismatches 80; Indels 8 29; Gaps 11;	
Qy	21 NGTSONISSLTSNPKQQSYKDIENK-----VKSLYFNRGISDIDLRSKQAKYTVH 74
Db	502 NKESKNIESENTDVKNKESENEDVNKEAENKDVKNDVK-NKEAE-NID 559
Qy	75 FKNGTRVVDLK-AGHTADLINTSDIKALSVNVDTK-----QVQDEKAANVQVPT 127
Db	560 AEINEDDENTDVKNRDENEDEDNTDVKNKESENINTVNDAENTHVKNKESK-NVDAENT 618
Qy	128 ITVNGTSONI-LSNLTEK---KNOQISYKDLN-----NVKSVLKSNRGITDVDLRLS 176
Db	619 YVTKNKDAENTHVKNKESKNIDVKNKAENKTENTDVKNDAENIDAENEDATDVK-N 677
Query Match	11.1%; Score 113; DB 2; Length 1828;
Best Local Similarity	21.0%; Pred. No. 48;
Matches 46; Conservative 42; Mismatches 81; Indels 42; Gaps 9;	
Qy	16 YITVNGTSONI-LLSQTTFNPKQQSYKDIENPKVSLYFNARGISDIDLRSKQAKYTVH 74
Db	64 YAKNVTNKKLESKILLNAKIDENS-SLQD1KNTKTKQV---KEALNSLSTCKERQKEQQ 118
Qy	75 FKNGTRVVDLKAGHTAD---LINTSDIKAIYN-----VDTKQVTDKREAKANVQVPT 127
Db	119 NQDKTTLDKWRLDFAAQELKALINSKQSKVSDTTKAVEVLTQKTTTQSATQVLO 178
Qy	128 I-TVNGTSONISSLNTFKKQ-----ISYKDLENNPKVSLKSN 165
Db	179 VQTKTKEATQPKKQOGENEENPKQAKBLTDYTANDLTKDIAKAKAE--KSI 235
Qy	166 RGITDVDLRSKQAKTIVNPKANGTKVLDK 196
Db	236 EKVSDINNSS---FISDIQQATKLIDAK 262
RESULT 33	
ID Q7RR45	PRELIMINARY;
AC Q7RR45;	PRT; 2341 AA.
DT 01-MAR-2004	('T'EMBLrel. 26, Created)
DT 01-MAR-2004	('T'EMBLrel. 26, Last sequence update)
DT 01-MAR-2004	('T'EMBLrel. 26, Last annotation update)
DB Hypothetical protein.	
GN Name=py00892;	
OS Plasmidium yoelii.	
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
NCBI_TaxID=73235;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=99102612; PubMed=9847359;	
RA Aronso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;	
RT "The genome of Melanoplus sanguinipes entomopoxvirus."	
RL J. Virol. 73:531-552 (1999).	
DR EMBL; AF063866; AAC976771; -.	
PIR; T28317; T23317.	
KW Hypothetical protein.	
SQ SEQUENCE 112 AA; 134265 MW; F155DA1D5A3FETD1 CRC64;	
Query Match	11.0%; Score 112; DB 2; Length 1127;
Best Local Similarity	23.3%; Pred. No. 32;
Matches 47; Conservative 40; Mismatches 81; Indels 34; Gaps 9;	
Qy	20 VNGTSONISSLTFN-KNQISYKDIENPKVSLYFNARGISDIDLRSKQAKYTVHFKNG 78
Db	177 VSSDEKQOLIEQYKNNKEEFKNDNVQEE---NPKQDELNKLDESKEFKIKOB 233
Qy	79 TTKRVVDLKAGHTADLINTSDIKAIYNPKVSDTTKQVQDK-EAKAN-----QVQVPTT 129
Db	234 LNKTKDK --- QEEELKKLNDKEINFNIDEQKLQDINSKINTLNENIKGWNLYTET 289
Qy	130 VNGTSONISSLNTFKKQOISYK-----LSNRYKSVL---LSNRYGITDVDLRSK 177
Db	290 KNKISN --- LQNELLNQDSTKISLDEQKLDELDNNINNITSLYNKSNTKINTNIQQLLES 347
Qy	178 QAKFTVNFKNPQKVKUDIKAGI 199

Db	348 S---LTDFFNNANININEKSKI 366	: : : : : : :	Q65HY4;	AC DT 25-OCT-2004 (T-EMBLrel. 28, Created)
				DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
				DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
				DE Hypothetical protein (Heterodimeric kinase, homodimeric).
				GN Name=cyk1; ORFNames=BL00655; BL02454;
				OS Bacillus licheniformis DSM 13.
				OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; NCBI_TaxID:279010;
				OX RN [1]
				RP RP SEQUENCE FROM N.A.
				RC RX STRAIN=DSM 13;
				RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich A., Gottschalk G.;
				RA Baumeier S., Hennig A., Liesegang H., Metzler R., RA "The Complete Genome Sequence of <i>Bacillus licheniformis</i> DSM13, an Organism with Great Industrial Potential." RT RT J. Mol. Microbiol. Biotechnol. 7:204-211(2004). RL RN [2]
				RP RP SEQUENCE FROM N.A.
				RC RX STRAIN=ATCC 14550;
				RA Rey M.W., Ramalya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olesen P.B., RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., RA Berkar R.M.; RA
				RT RT "Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species." RL Genome Biol. 5:R77-R77(2004).
				DR DR EMBL; AB017333; AAU041301; -.
				DR DR EMBL; CP000002; AAU23976.1; -.
				KW Hypothetical protein; Kinase.
				SEQUENCE 483 AA; 55528 MW; BC070BB08FC61BEE7 CRC64;
				Query Match 10.9%; Score 111; DB 2; Length 483;
				Best Local Similarity 20.9%; Pred. No. 14;
				Matches 51; Conservative 36; Mismatches 63; Indels 94; Gaps 11;
				Qy 18 ITVNGSONISSLTTNPKNQQLSYD-L-EENKVSVLYFNFRGISDIDRLRSQAKYTVHFK 76
				Db 22 LVLNHTVKVVI-WSSNEKIVTSVLVELKKNSTTYVN-----QAFLINHY 65
				Qy 77 NGTKRYVDSL-----KAGIHTAD-LINTSDIKAI-----VVNDTPTKQVQDKREA 118
				Db 66 NNELYFGDADMVDNHNHSTGNSNGVYTGDALLSSDQVFSSRSDELDQQAIGKTA 125
				Qy 119 -----KANVQVPPYTITNGTSQNLNSLITEKRNQKQISYK-----152
				Db 126 YHTYTNRKAKVFFSYPPVTEGTQVGT----LRFSKNFDLILYKQSGBEILDIVFYIAIFV 182
				Qy 153 -----DLIENRNVSKRHTIPVVKLTDATSQQK-----NKFTNFNRG 188
				Db 183 AAFLFSYILSRHITIPVVKLTDATSQQK-----KGKLDMDIHFNRKDEIGQLAVNENDM 236
				DB Hypothetical protein.
				GN ORFNames=PR10_0265;
				OS Plasmodium falciparum (isolate 3D7).
				OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
				NCBI_TaxID:36329; RN [1]

RESULT 35

Q9ZHL0 PRELIMINARY; PRT; 4919 AA.

AC Q9ZHL0; Q7BY44; PRELIMINARY; PRT; 4919 AA.

DT 01-MAY-1999 (T-EMBLrel. 10, Created)

DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)

DE Large supernatant protein 2.

OS Haemophilus ducreyi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.

RN [1] NCBITaxonID:730;

RP SEQUENCE FROM N.A.

RC STRAIN=350000;

RX MEDLINE=99030326; PubMed=9811662;

RA Ward C.K., Lumb B.S.R., Latimer J.L., Cope L.D., Hansen E.J.,

RT "Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein";

J. Bacteriol. 180:6013-6022(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=350000P / ATCC 700724;

RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Munger R.,

RA Johnson L., Nguyen D., Wang J., Forrest C., Hood L., InterPro: IPR0086138; Haemagg_act_N.

DR Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF057696; AAC79761.1; -.

DR EMBL; AB01754; AAC79612.1; -.

DR PIR; T31105; T31105.

DR GO: GO:0004197; F: cysteine-type endopeptidase activity; IEA.

DR GO; GO:000405; P: pathogenes; IEA.

DR InterPro: IPR0086119; Fil haemagg.

DR InterPro: IPR0086138; Haemagg_act_N.

DR InterPro: IPR0086151; Peptidase_C58.

DR InterPro: IPR006473; Peptidase_C58_yt.

DR Pfam; PF05594; Fil haemagg; 10.

DR Pfam; PF05860; Haemagg_act; 1.

DR Pfam; PF03543; Peptidase_C58; 1.

DR TIGRFAMs; TIGR01901; adhes_NP0K; 1.

DR TIGRFAMs; TIGR0586; yopT_cys_prot; 1.

XW Complete proteome.

SQ SEQUENCE 4919 AA; 542602 MW; 5779201455CA69A0 CRC64;

Query Match 11.0%; Score 112; DB 2; Length 4919;

Best Local Similarity 25.7%; Pred. No. 1.7e+02;

Matches 52; Conservative 29; Mismatches 67; Indels 54; Gaps 10;

Db 633 SLNASHNVTLNNSK---LSA-----QKADIRAVNLNTTELAKNLIN--S 677

Qy 18 ITVNGTSQNLNSLITEKRNQKQISYK-----NQKISYKDLENNNSVTKNSNRGKTD 170

Db 678 TTITNGTGTAGPANTKLNKEKLLAEQNNTVNGSHYENKGDIVSKRQATV- 736

Qy 126 YDRLRSKQAKETVNFNGTKKV 192

Db 737 ---FSKNSDFT---SNGSKLV 751

RESULT 36

Q65HY4 PRELIMINARY; PRT; 483 AA.

Db Q8IJJD3 PRELIMINARY; PRT; 1811 AA.

ID Q8IJJD3 ID Q8IJJD3; PRELIMINARY; PRT; 1811 AA.

DT 01-MAR-2003 (T-EMBLrel. 23, Created)

DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN ORFNames=PR10_0265;

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID:36329; RN [1]

Db 177 QPFLSKKREGKRISTNPEIJKENVD 203

RESULT 40
QBRBU3 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 ID QBRBU3 PRELIMINARY; PRT; 398 AA.
 AC QBRBU3 ;
 DT 01-JUN-2002 (TrEMBLref. 21; Created)
 DT 01-JUN-2002 (TrEMBLref. 21; Last sequence update)
 DT 01-MAR-2004 (TrEMBLref. 26; Last annotation update)
 DE Predicted transposase.
 GN OrderedLocusName=TRTE0715;
 OS ThermomaeroBacter tangcongensis.
 OC Bacteria; Firmicutes; Clostridia; ThermomaeroBacteriales;
 OC ThermomaeroBacteriaceae; ThermomaeroBacter.
 OX NCBI_TaxID=119072;
 RN (1)
 RP SEQUENCE FROM N.A.

RC STRAIN=MB4;
 RX MEDLINE=2192816; PubMed=1199736; DOI=10.1101/gr.219302;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of the T. tengcongensis genome.";
 RL Genome Res. 12:689-700 (2002).
 DR EMBL; AE013039; AACM3977.1;
 DR InterPro; IPR001959; Transposase_2.
 DR InterPro; IPR010095; TspaseT_teng_C.
 DR Pfam; PF01385; Transposase_2_1.
 DR Pfam; PF02782; Transposase_35; 1.
 DR TIGRFAMs; TIGR01766; tspaseT_teng_C; 1.
 KW Complete proteome.
 SQ SEQUENCE 398 AA; 46552 MW; 6268889A16A05AB CRC64;

Query Match 10.8%; Score 110; DB 2; Length 398;
 Best Local Similarity 24.5%; Pred. No. 13; Mismatches 78; Indels 36; Gaps 8;
 Matches 47; Conservative 31; Mismatches 78; Indels 36; Gaps 8;
 Qy :|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 116 NGRSVAIFT-----NQQCKTKDGHLSFPKTNLKLKTRITGKLEYRIIPGSVYVIEIV 169
 Qy 65 LSKQAKYTVHFKNGTRAVVDKAGIHT-ADLINTSDIKAIISVNVDITKKQYKDKEAKANVQ 123
 Db 170 YEKE---VVERKKPSKTRIAGDGLANFVILVANNIGKPIVINGKTKSINQYNNKKAE 226
 Qy 124 VPYTIVNGTSQNLISNLTFCKNQOQISYKDLLENNYVKSLKSNRGTTDVDLRLSKQAQFTV 183
 Db 227 LMSYVEDRGTS-NRIEKTTLKRNNKI--KDLMHKTSRFVNWKQHDID-----TIVI 276
 Qy 184 NFKNQGKVKVIDL 195
 Db 277 GYNSGMKQEIEL 288

Search completed: March 16, 2005, 10:39:41
 Job time : 177 SECs

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OM protein - protein search, using bw model		31	97.5	9.6	1207	2	S27954
Run on:	March 16, 2005, 10:36:37 ; Search time 41 Seconds (without alignments) 469.350 Million cell updates/sec	32	97	9.5	647	2	H89988
Title:	US-10-041-775-2	33	97	9.5	3890	2	C89921
Perfect score:	1016	34	96.5	9.5	408	2	AC1098
Sequence:	1 MRSHHHHHGSQLPYTTV.....FTYNFKNGTKKVIDKAGIV 200	35	96	9.4	295	2	G97827
Scoring table:	BLOSUM62	36	96	9.4	690	2	E8A945
Scoring table:	Gapop 10.0 , Gapext 0.5	37	95.5	9.4	377	2	H82882
Searched:	283416 seqs, 96216763 residues	38	95.5	9.4	521	2	E70129
Total number of hits satisfying chosen parameters:	283416	39	95.5	9.4	52	2	F9063
Minimum DB seq length: 0		40	95	9.4	682	2	C97183
Maximum DB seq length: 2000000000		41	95	9.4	298	2	C97183
Post-processing: Minimum Match 0%		42	95	9.4	746	2	T47237
Post-processing: Maximum Match 100%		43	95	9.4	1039	2	D97985
Database :	PIR_79;*	44	95	9.4	1039	2	H71605
	1: PIR1:*	45	94.5	9.3	645	1	SUBSMP
	2: PIR2:*						
	3: PIR3:*						
	4: PIR4:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description		
-	-	-	-	-	-	hypothetical prote	RESULT 1
1	318	31.3	121	2 S15765		hypothetical prote	S15765
2	210	20.7	144	2 F89465		hypothetical prote	
3	146.5	14.4	141	2 H90016		hypothetical prote	
4	136	13.4	106	2 H89982		truncated map-w pr	
5	114.5	11.3	640	2 H8226		DNA topoisomerase	
6	114.5	11.3	1272	2 H82226		conserved hypothetical	
7	112	11.0	1127	2 T28317		ORF MSV15.6 hypothe	
8	112	11.0	4919	2 T31105		hypothetical prote	
9	107	10.5	483	2 A69745		hypothetical prote	
10	107	10.5	520	2 E97813		WASP, N-WASP, MENA	
11	104.5	10.3	297	2 C7031		hypothetical prote	
12	103.5	10.2	609	2 S57378		hypothetical prote	
13	103.5	10.2	1778	2 AP1116		internalin protein	
14	103.5	10.2	3216	2 C90538		hypothetical prote	
15	103	10.1	688	2 T43783		probable cell surf	
16	102.5	10.1	410	2 AH1484		surface membrane P	
17	102.5	10.1	624	2 PC6003		filamentous hemag	
18	102.5	10.1	4152	2 T31102		hypothetical prote	
19	102	10.0	796	2 T43782		high-molecular-weight	
20	101	9.9	1536	2 A43055		B. subtilis YabE p	
21	100.5	9.9	405	2 AB1461		hypothetical prote	
22	100.5	9.9	4550	2 T18440		hypothetical prote	
23	100	9.8	251	2 H1293		RIF2 protein - Yea	
24	100	9.8	533	2 S52102		conserved hypothetical	
25	99.5	9.8	226	2 E69359		hypothetical prote	
26	98.5	9.7	888	2 E82885		surface-layer 125k	
27	98.5	9.7	1176	2 A33056		conserved hypothetical	
28	98	9.6	450	2 E69394		conserved hypothetical	
29	98	9.6	522	2 D72349			
						ALIGMENTS	
						Query Match	31.3%;
						Best Local Similarity	76.5%;
						Matches	62;
						Conservative	9;
						Mismatches	10;
						Indels	0;
						Gaps	0;
						A;Cross-references:	UNIPROT:P21223; EMBL:X13404; PIDN:CAA31768.1; PID:946587
						A;Cross-references:	<PRO>
						A;Residues:	1-121 <PRO>
						C;Species:	Staphylococcus aureus
						C;Date:	04-Dec-1992 #sequence_revision 04-Dec-1992
						C;Accession:	S15765; S04522
						R;Protein:	S.J.; Korribium, J.; Kreiswirth, B.; Moghazeh, S.L.; Eisner, W.; Novick, R.P.
						Nucleic Acids Res:	17, 3305, 1989
						A;Title:	Nucleotide sequence: the beta-hemolysin gene of Staphylococcus aureus.
						A;Reference number:	S15765; MUID:89263748; PMID:2726469
						A;Accession:	S15765
						A;Status:	translation not shown
						A;Molecule type:	DNA
						A;Residues:	1-121 <PRO>
						C;Cross-references:	
						Qy	4 SHHHHHHGSQIPIPTVNTGTSNIIQLSSLTENKQNSYKTDENKVSVLVNNGISDIDL 63
						Db	41 SLHGGSKVHVYATVNGTSQNLQSSLTENQNNTSYKTDLEDRVKSVLSDRGISDIDL 100
						Qy	64 RLSKQAKQTVTFVKNGKVRVD 84
						Db	101 RLSKQAKQTVTFVKNGKVRVID 121
						RESULT 2	
						F89865	
						hypothetical protein SA0841 [imported] - Staphylococcus aureus (strain N315)	
						C;Species:	Staphylococcus aureus
						C;Date:	10-May-2001 #sequence_revision 10-May-2001
						C;Accession:	F88865
						R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, M.; Mizutani, Y.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	
						Lancet:	357, 1225-1240, 2001
						A;Title:	Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
						A;Reference number:	A89758; MUID:21311952; PMID:11418146
						A;Accession:	F88865
						A;Status:	preliminary
						A;Molecule type:	DNA
						A;Residues:	1-144 <PRO>
						C;Cross-references:	UNIPROT:Q90VA9; GB:BA000018; PIDN:913700785; PIDN:BA842081.1; GSPDB:C
						A;Experimental source:	strain N315
						C;Genetics:	
						A;Gene:	SA0841
						Query Match	20.7%;
						Best Local Similarity	44.3%;
							Pred. No. 1-2e-07;

RESULT 5		
Qy	72 TVHFNGKTRVVDLKAGIHTADLINTSDKAISVNV 107 S35734	
Db	69 KVFNGSSKVVDLKTEYKDERVKATDIKVDIEL 104 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B N; Alternate names: DNA gyrase chain B C; Species: Spiroplasma citri C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ter C; Accession: S35734 R; Ye, F.; Lalorjet, F.; Bove, J. Submitted to the EMBL Data Library, December 1992 A; Description: Nucleotide sequence and genetic organization A; Reference number: S35732 A; Accession: S35734 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-640 <YPE> A; Cross-references: UNIPROT:P34031; EMBL:219108; NID:9732 C; Genetics: A; Genetic Code: SGCG3 C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chaperone C; Keywords: antibiotic resistance; ATP; heterotetramer	
Query Match		
Qy	9 HHGSQLIPPTVNTGTSQNLLSSLTFLPKNNQQI-----SY Db	145 HNGGQLITPPKEVGSSTSETGTIVTFLPDKIFKETTIFSFSF
Qy	60 DIDIRLSKQAKYTH-FNGTK-RVVDLKAGIHTADLINT Db	205 LVDLREEDSEKTVLYQFNNGKTDYVLELNKTCTP---LI
Qy	118 AKANQVPPYTNTG-TSONILS---NH----TFKKQKQ Db	252 ---NIVVEFGQLYNDNN-SVNIFFCNNVNTHEGGTHEBGA
Qy	166 RGTTDVLRLSKQAKFT-VNFKNGTKVYIDLK 196 Db	309 KGNEQ-----KFTWDDIKEGMTIISIR 331
RESULT 6		
Qy	H82926 conserved hypothetical UU143 [imported] - Ureaplasma urealyticum C; Species: Ureaplasma urealyticum C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #ter C; Accession: H82926 R; Glass, J.I.; Leffowitz, E.J.; Glass, J.S.; Heiner, C submitted to GenBank, February 2000 A; Description: The complete sequence of Ureaplasma ure A; Reference number: A82870 A; Accession: H82926 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1272 <GLA> A; Cross-references: GB:AE02115; GB:AF222894; NID:g689 A; Experimental source: serovar 3; biovar 1 C; Genetics: A; Genetic code: UUU143 A; Gene code: SGCG3	
Query Match		
Qy	14 IPYTITVNGTSQNLLSSLTFLPKNNQQI-----SYDENKVSVY	

Db	637 IPYSL-----RNLI-SLTLLHREAYIK--HNATNGFLYNTITNSKDNFLNKKNSKSY 687	Query Match Score 112; DB 2; Length 4919;
Qy	74 HFKN-----GTVVVDLKG-----IHTADLTNTSDIKAIISVNVT-----109	Best Local Similarity 11.0%; Pred. No. 38;
Db	688 HLNLSLIAILAKDDEGLKK---D8AGFFLEKDLNDDFDNINNPDEDIVFVNDLDELDPNLY 745	Mismatches 52; Conservative 29;
Qy	110 KQKVKDKR-AKANQVQPTTYTNGTSQJNLSNLTKENQISYKDKLENNSVKSLSKNSRGI 168	Indels 54; Gaps 10;
Db	746 ESQLVDKMRRSVIVIPSYKVI-IKQHILEDVEFSINYALGSSEAYNHIOQIKS--- 800	Matches 52;
Qy	169 TDVLRLSKQAKETVNFNGTKVQKVIDLK 196	Query Match Score 112; DB 2; Length 4919;
Db	801 -----QLKENV-FNLGSKVKEVK 818	Best Local Similarity 25.7%; Pred. No. 38;
RESULT 7		
T28317	ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus	Query Match Score 112; DB 2; Length 4919;
C; Species: <i>Melanoplus sanguinipes</i> entomopoxvirus	C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004	C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: T28317	C; Accession: A69745	C; Accession: A69745
R; Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.	R; Kunst, F.; Ogasawara, I.; Albertini, A.M.; Allione, G.; Azevedo, V.; Berger, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.	R; Kunst, F.; Ogasawara, I.; Albertini, A.M.; Allione, G.; Azevedo, V.; Berger, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
J; Virol. 73, 533-552, 1999	Nature 390, 249-256, 1997	Nature 390, 249-256, 1997
A; Title: The genome of <i>Melanoplus sanguinipes</i> entomopoxvirus.	A; Authors: Bouliger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Huilo, M.P.; Koetter, P.; Koningschein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidous, A.; Lardinois, Y.; M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Pohl, T.M.; Portetelle, Rieger, M.; Rivoltella, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Schleich, S.; Schreuter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serov, akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Uchiyama, T.; Winter, P.; Wipat, A.; Yamamoto, K.; Yashima, K.; Yata, K.; Yoshida, K.	A; Authors: Bouliger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Huilo, M.P.; Koetter, P.; Koningschein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidous, A.; Lardinois, Y.; M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Pohl, T.M.; Portetelle, Rieger, M.; Rivoltella, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Schleich, S.; Schreuter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serov, akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Uchiyama, T.; Winter, P.; Wipat, A.; Yamamoto, K.; Yashima, K.; Yata, K.; Yoshida, K.
A; Accession: T28317	A; Status: preliminary; translated from GB/EMBL/DDBJ	A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ	A; Molecule type: DNA	A; Molecule type: DNA
A; Residues: 1-1127 <A>O>	A; Cross-references: UNIPROT:Q9YWT6; EMBL:AF063866; NID:94049647; PIDN: AAC97677.1; PMID:9843759	A; Cross-references: UNIPROT:Q9YWT6; EMBL:AF063866; NID:94049647; PIDN: AAC97677.1; PMID:9843759
A; Genetics: MSV156	A; Genetics: MSV156	A; Genetics: MSV156
Qy	20 VNGTSQNLSSLTFN-KNOQISYKDIENKVSVLYFNRGISDIDLRSKQAKYTVMFKNG 78	Query Match Score 112; DB 2; Length 1127;
Db	177 VSSDEKLQIEQIYKNNKEFEKNTVQKESI--NKQKODEBLNKLUDESKKEFIKKQEE 233	Best Local Similarity 23.3%; Pred. No. 6.4;
Qy	79 TKVVDLKGAGIHTADLTNTSDIKAIISVNVTDPKKQVQDK-EAKAN-----QVQPWIT 129	Mismatches 40; Conservative 47; Indels 34; Gaps 9;
Db	234 LNKTIDRK---QEELKKLNDKEINPVIDERQKLLDQINSKINTLNENIKGVMLYET 289	Matches 43; Conservative 37; Mismatches 40;
Qy	130 VNCTSONTSLNLTFKKNQISYKD-----LNNYKSVL---KSNRGITDVDLRSK 177	Query Match Score 107; DB 2; Length 483;
Db	290 KNKISN-LQNETLANKDSTIKSLDEKQKLLDQEDKNNNNTSLYNKNTNQQLES 347	Best Local Similarity 22.4%; Pred. No. 4.9;
Qy	178 QAKPTVNFNGTKVQKVIDKAGI 199	Mismatches 37; Mismatches 43;
Db	348 S---LTDFFNNANTINNIELSKI 366	Indels 50; Gaps 7;
RESULT 8		
T31105	hypothetical protein 2 - Haemophilus ducreyi	Query Match Score 10.5%; DB 2; Length 483;
C; Species: <i>Haemophilus ducreyi</i>	C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004	C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C; Accession: T31105	R; Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.	C; Accession: T31105
J; Bacteriol. 180, 6013-6022, 1998	J; Bacteriol. 180, 6013-6022, 1998	J; Bacteriol. 180, 6013-6022, 1998
A; Title: <i>Haemophilus ducreyi</i> secretes a filamentous hemagglutinin-like protein.	A; Reference number: 220984; PMID:99030322; PMID:9811662	A; Reference number: 220984; PMID:99030322; PMID:9811662
A; Status: preliminary; translated from GB/EMBL/DDBJ	A; Status: preliminary; translated from GB/EMBL/DDBJ	A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA	A; Molecule type: DNA	A; Molecule type: DNA
A; Residues: 1-4919 <W>R>	A; Residues: 1-4919 <W>R>	A; Residues: 1-4919 <W>R>
C; Cross-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:93929021; PIDN: AAC7	C; Cross-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:93929021; PIDN: AAC7	C; Cross-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:93929021; PIDN: AAC7
A; Gene: 1spaa	A; Gene: 1spaa	A; Gene: 1spaa
Db	304 VKKISPSKVTLH 315	Query Match Score 107; DB 2; Length 483;

RESULT 10
 E97813 WASP, N-WASP, MENA protein homolog [imported] - Rickettsia conorii (strain Malish 7)
 C;Species: Rickettsia conorii
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: E97813
 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
 Science 293, 2093-2098, 2001
 A;Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.
 A;Reference number: A977000; PMID:21442074; MUID:11557893
 A;Accession: E97813
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-520 <KUR>
 A;Cross-references: UNIPROT:Q92H62; GB:AE006914; PIDN:ANL03447.1; PID:gi15620016; GSDB:G
 C;Genetics:
 A;Gene: RC9909

Query Match Score 10.5%; Length 520;
 Best Local Similarity 19.5%; Pred. No. 5.4;
 Matches 47; Conservative 49; Mismatches 77; Indels 68; Gaps 10;

Qy 10 HGSQIP---YITVNGTSONISSLTFENPKQISY---KDIENRKVSKVLYFNRGISD 60
 Db 55 HNRSLPWFKRFYKTVSNKYLIJKSEBQLTNEAIKVNKKILXIDNKI---INTAEKS 109

Qy 61 IDRLRSKQAKTYTHEKGNTKRVVDLK---AGIHTADLI---95
 Db 110 APIKQALQEEIEKNFKDLTK--DLSKDQRARLSEEFFSYKSKEPFSALHMTPNPLQFIN 167

Qy 96 ---N-SDIAKISVNDTKEKQVKDKEAKANQVQPYT-I-TVNGTSONI 137
 Db 168 AERLEKQNSLMATKQNQIANSNSKKEIQTQWAEIETRAEVPHTEFFKLNNIWQV 227

Qy 138 LSNLTFKRNQQISYKODLENVVKSVLKSNSNRGTTDVLRSK-QAKTFTNFKNGTKKVIDLK 196
 Db 228 -KNVFVNNSQVLAQNKESENTRIK---IDEQYKTKHKFEBELIERNKNIKII 279

Qy 197 A 197
 Db 280 A 280

RESULT 11
 C70231 hypothetical protein BBG01 - Lyme disease spirochete plasmid G/1p28-2
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)
 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C;Accession: C70231
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanlon, M.; Vugt,
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Hatch, B.
 A;Authors: Smith, H.O.; Venter, J.C.
 A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A;Reference number: A70100; MUID:98065943; PMID:9403685
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-297 <KUR>
 A;Cross-references: UNIPROT:O50726; GB:AE000786; PIDN:g2690008; PID:gi66073.1; PID:9269
 A;Experimental source: strain B31
 C;Genetics:
 A;Plasmid
 C;Superfamily: *Borrelia burgdorferi* hypothetical protein BBK01

Query Match 10.3%; Score 104.5; DB 2; Length 297;
 Best Local Similarity 25.9%; Pred. No. 4;
 Matches 52; Conservative 36; Mismatches 64; Indels 49; Gaps 12;

Qy 16 YTITVNGTSONISSLTFENPKQISYKODLENVVKSVLKSNSNRGTTDVLRSK-QAKTFTNFKNGTKKVIDLK 196
 Db 8 YTLLMGGLMSCNLDSKLSSNKEQNNNNVKEVSNSVQ----EDGLNLDSNQEOKSFT 62

RESULT 12
 S57378 hypothetical protein YOJ091w - yeast (Saccharomyces cerevisiae)
 A;Molecule type: DNA
 N;Alternative names: hypothetical protein O0932
 C;Species: Saccharomyces cerevisiae
 C;Accession: S57378; S56785; S50414
 R;Zunstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
 A;Title: A 29-425 kb segment on the left arm of yeast chromosome XV contains more than t
 A;Reference number: S57374; PMID:96021609; PMID:9533473
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q12411; EMBL:X83121; NID:9600461; PIDN:CAA58188.1; PID:96004
 R;Zunstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S66775
 A;Accession: S66778
 A;Molecule type: DNA
 A;Cross-references: EMBL:Z744833; NID:gi1419935; PID:e251887; PID:gi1419936; MIPS:YOL091w
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: SGD:SPO21
 A;Cross-references: SGD:S0005451
 A;Map position: 15L

Query Match 10.2%; Score 103.5; DB 2; Length 609;
 Best Local Similarity 24.4%; Pred. No. 11; Mismatches 56; Indels 69; Gaps 11;
 Matches 51; Conservative 29; Mismatches 56; Indels 69; Gaps 11;

Qy 24 SQN---TLLSLTENKQISYKDI--EN-KVKSVL-----YFNRGISDIDRLRSKQAKYT 72
 Db 302 SONDKILKLETTNKAYTKVKEVSLENKKIKEAFKELDNESYNH----DEELLKKYKT 356

Qy 73 VHFKGNTKRVVDLKAGHTADLINTSDIKAISVNDTKEKQYDKEAKAN----121
 Db 357 -----RETLDVRNRCOLIDQNFLKKSYNELQEVNATNFKSLFKE 400

Qy 122 --QVQPTTIVNGT---QNLISNLTFKQKQ---ISYKDLENVVKSVLKSNSNRGTTDVLRSK-QAKTFTNFKNGTKKVIDLK 196
 Db 401 KYAKLADSITELNSTKREAGLENFTECNLKEICLKYK---KNIENISNTNRLQN-
 Qy 172 DLRLSKQAKTFVNFNGTKKVIDLK 196
 Db 457 -----SFNERKVKYDLR 469

RESULT 13
 AF1116 internal proteins, probable peptidoglycan bound protein (LPXTG motif) homolog lmo0333
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AF1116
 R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001				
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, O.; C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boiland, J.A.; Voss, H.; Wehland, A.;Title: Comparative genomics of Listeria species.				
A;Reference number: AB1077; MUID:2153779; PMID:11679659				
A;Accession: AP1116				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-1778 <GLA>				
A;Cross-references: UNIPROT:QBYA32; GB:NC_003210; PIDN:CAC98412.1; PMID:gi16409711; GSPDB: C;Genetics:				
A;Gene: Imo0333				
Query Match 10.2%; Score 103.5; DB 2; Length 1778;				
Best Local Similarity 20.2%; Pred. No. 42;				
Matches 50; Conservative 38; Mismatches 73; Indels 87; Gaps 11;				
Qy 17 TITVNGTQNISLSSTFNKNQQISYKTDIENKVSKTYFNRGISDID----- 62				
Db 1014 TVTNKDPPISAKT----EITDKFSKKTEAF----LDDDAADTNDSIVTSNFA 1063				
Qy 63 -LRLSKQAKYTTHEKNGTKRVDLKGIAHTADLINTSDIKAINVNVTDTKQ----- 112				
Db 1064 TAVNLKDAGDTYTVLNSNS--DGAVGTPTAIIHVKEKIAITSTNTAQYEYAKIN 1120				
Qy 113 ---VKDREBAKAN----VQVP--YTITVNGTQN----- 136				
Db 1121 ETQFLKDYHASINASPTTAVLESDEFTVVKLDVPGTYTVTTATNEDEGGVASPKEVSVIV 1180				
Qy 137 -----ILSNLTFKRNQKISYKTDLENNVKSYLK-SNRGIT--DVDLRLSKQAKFTV 183				
Db 1181 RKIPAPETTADKEITYPKDFEVESEAPLNIDIHATISDRNVAITSNSFSTDVNLNKAGDVTY 1240				
Qy 184 NFKNQTKK 191				
Db 1241 TL-NATNE 1247				
RESULT 14				
C90538				
A;hypothetical protein MYPU_2110 [Imported] - Mycoplasma pulmonis (strain UAB CTIP)				
C;Species: Mycoplasma pulmonis				
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004				
C;Accession: C90538				
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001				
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm				
A;Reference number: A99512; MUID:21267165; PMID:11353084				
A;Accession: C90538				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-3216 <KUR>				
A;Cross-references: UNIPROT:Q98Q93; GB:AL445566; PID:gi14089624; PIDN:CACT13384.1; GSPDB: C;Genetics:				
A;Gene: MYPU_2110				
A;Genetic code: SG3				
Query Match 10.2%; Score 103.5; DB 2; Length 3216;				
Best Local Similarity 25.6%; Pred. No. 86;				
Matches 50; Conservative 33; Mismatches 83; Indels 29; Gaps 7;				
Qy 16 YTTVNGTQNISLSSTFNKNQQISYKTDIENKVSKVL-----YFNRGISDIDLRSKQ 69				
Db 201 YEIKV--SSVNVASLTSVNLNLSRNGIQKEVCTIIGIPIATSKVQDANDVPLKD 258				
Qy 70 KTYVHFKNGTKRVDLKGIAHTADLINTSDIKAI-----SVNVDTKEVQDKEAKANTQVPTY 127				
Db 259 NLVIVSYNGNIDSPLDLINKV--ASQISLNDFHPIVPSDNVDVYKUVSIKASEQNQQ-SVI 315				
Qy 128 ITVNGTQNISLSSTFNKNQQISYKTDIENKVSKVLKSNGCITDVRLSLQAKFTVNFKN 187				

Db	316	LTIKTSKTHGNNAPIYSKDTYEVNLLSSDMFELLYNNR-----YEANFSVNPQT	365
Qy	188	GTKK-----VIDLK 196	
		:	
Db	366	QAKRSAYETISDLK 380	
RESULT 15			
T43783	hypothetical protein 688 [Imported] - slime mold (<i>Dictyostelium discoideum</i>) mitochondrial C;Species: mitochondrial <i>Dictyostelium discoideum</i>		
C;Accession: T43783	Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004		
Ri;Ogawa, S.; Yoshino, R.; Angata, K., Bi, M.; Iwamoto, M.; Kuroe, K.; Matsumoto, K.; Morio, A.;Description: The mitochondrial DNA of <i>Dictyostelium discoideum</i> . Complete sequence, ger A;Reference number: Z222666	A;Accession: T43783		
A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Molecule type: DNA		
A;Residues: 1-688 <OGA>	A;Cross-references: UNIPROT:Q34312; EMBL:AB000109; PIDN:BA78086.1		
A;Genetics:	C;Superfamily: NADH dehydrogenase (ubiquinone) chain 11		
C;Keywords: mitochondrial			
Query Match	10.1%	Score 103; DB 2; Length 688;	
Best Local Similarity	24.3%;	Pred. No. 14;	
Matches	49;	Conservative 41; Mismatches 48; Indels 64; Gaps 13;	
Qy	26 NILSSLTENKNOQISYKDILENKVSKVSYFNRGI-----SDIDLRISKQAKYTVPFKNGT 79		
Db	518 NVLVSIDSNEVQ-----VTKNKNVIV--QGIIINDKPFENKIDYL--PSKHYFEDFEGD 567		
Qy	80 KRYVDLKGHTADINT----SDDAISAIKVNVDTDKQVKDREKAANVQPVTTVNTGSQ 135		
Db	568 REV-----YMTTIGQRSETEKLSTISGKWK--IKENSMIGIQLMY----- 605		
Qy	136 NILSN--LTFFKRNQO---ISYKOLENNVKSVLKSRNGI-----TDVDLRLSKQ 178		
Db	606 --LNKKEMTRIKEEQDKIISLYRMKEKEERKIKVNVKTINNIENYMTDINRLSKN 663		
Qy	179 AKFTPNFKNGTKVYIDLKAGIY 200		
Db	664 LMTGQLRK-EKKI-MENGW 682		
RESULT 16			
AH1484	probable cell surface protein (LPXTG motif) [Imported] - <i>Listeria innocua</i> (strain Clip1 C;Species: <i>Listeria innocua</i>		
C;Accession: AH1484	Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004		
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dubourget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, S.P.; Kreft, J.J.; Kuhn, M.; Kunst, F.; Kuraphat, G.; Madiueno, E.; Maitournam, A.; Ma, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.;Title: Comparative genomics of <i>Listeria</i> species.	A;Authors: Kreft, J.J.; Kuhn, M.; Kunst, F.; Kuraphat, G.; Madiueno, E.; Maitournam, A.; Ma, C.;Reference number: ABI077; MUID:2153729; PMID:11679669		
A;Accession: AH1484	A;Status: preliminary		
A;Molecule type: DNA			
A;Residues: 1-410 <GLA>			
A;Cross-references: UNIPROT:Q92EP3; GB:AL592022; PIDN:CAC95648.1; PMID:g16412844 ; GSPDB:C			
A;Experimental source: strain Clip1262			
C;Genetics:			
A;Gene: lin0415			
Query Match	10.1%	Score 102.5; DB 2; Length 410;	
Best Local Similarity	21.7%	Pred. No. 9;	

RESULT 20	Qy 53 -YFNRGISIDLRISKQAQTYVHFKNGTKRVDLKGAGHTADLINTSDIKAIISVNVDTKK 111	Db 149 VNTRATE-----ISLQNGTKKDKDTWTTKCKVSDILTEKNIK----LOKDD 190
A;Species: Haemophilus influenzae	Qy 112 QV---KDK--EAKANVQVPTTIVNGTQNQIISLNLTPEKQKQISYKDLENNVKSVLKSNR 166	Db 191 RVSPAKOSNLKEKMTVQTVY---VNSKAE-----KKNEQTKFETVYKEDDSLNLNGVE 239
C;Accession: A43855	Qy 167 GTTDDVDRLSKQKFTVNFKN 187	Db 240 KVQECKNGERKVBYNVTEN 260
R;Barenkamp, S.J.; Leininger, E.		
A;Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Ha		
darella pectussis.		
A;Reference: A43855		
A;Accession: A43855		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-1536 		
A;Cross-references: UNIPROT:Q48031; GB:U08876; NID:9475770; PIDN:AAA20527.1;		
A;Note: sequence inconsistent with the nucleotide translation		
A;Note: sequence extracted from NCBI backbone (NCBIN:89235; NCBIPI:89239)		
Query Match 9.9%; Score 101; DB 2; Length 1536;		
Best Local Similarity 23.9%; Pred. No. 51;		
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;		
Qy 3 GHSHHHHHGSQLPPTI-----TNYNGTSQNTLSSLTPKNOOISYKDIEENKVKS 51		
Db 863 GSDFDNH--QKPLTIKRDVINSGLNLAGGNIVNAGNLTVESN--ANFRAITNFTEN 917		
Qy 52 --LYFNRGISDI-----DLRLSKQAKTYVHFKNGTKRVDLKGAGHTADLNTS 98		
Db 91.8 GGFLDFNKSNIATKGARPKDIDNSKNSLTTNTSSSSTYRTII-----SGNTITKNG 970		
Qy 99 DIAKASVVDTTRKQ---VRODEKAANTQVPTTIVNGTQNQIISLNLTPEKQKQISYK 152		
Db 971 DLNTNEGSSTDTEMQIGGSVQSKEG-----NLTISSDKINITYKQTITKAGVGDENS 1022		
Qy 153 DLLENNVKSVLKSNRGTIDYDLRSKQAKFTVNFKNQGTMKVIDLKG 198		
Db 1023 DATNNANLTIKRELKLTDLNTSGNRAETAKDGS---DIRIG 1064		
Qy 82 VYDLKAGHTADLINTSDIKAIISVNVDTKK-----KEAKANVQVP- 125		
Db 1416 IKDIKNSEDIKIDKNDVSSYHLNKCCVNNSKSDTQDCPSSDDKNNNNIKRNKNIKTQ 1475		
RESULT 21		
A;subtilis YabE protein homolog lin00225 [imported] - Listeria innocua (strain Clip11262		
C;Species: Listeria innocua		
C;Accession: AB1461		
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karst, U.		
Science 291, 849-852, 2001		
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Title: Comparative genomics of Listeria species.		
A;Reference number: AB1077; PMID:21537279; PMID:11679669		
A;Accession: AB1461		
A;Status: Preliminary		
A;Molecule type: DNA		
A;Residues: 1-405 		
A;Cross-references: UNIPROT:Q92P81; GB:AU592022; PIDN:CAC95458.1; PID:916412644; GSPDB:G		
A;Experimental source: strain Clip11262		
C;Genetics:		
A;Gene: lin00225		
Query Match 9.9%; Score 100.5; DB 2; Length 405;		
Best Local Similarity 24.4%; Pred. No. 11;		
Matches 49; Conservative 32; Mismatches 67; Indels 53; Gaps 10;		
Qy 11 GSQIPY-----TIVNGTSQNTLSSL-----FVKNGQISYKD-----TENKVKSVL 52		
Db 89 GMEIKYLPARQVTFINDCTKVNWSKTKINVADLKDENITPRQDVNNVALDTLKNGLE 148		
Query Match 9.8%; Score 100; DB 2; Length 251;		
Best Local Similarity 25.4%; Pred. No. 6.6;		

Db	664	LLNSYKIRAIENLSTNKKIDNPPIKIVNDNGKPQLQI-HINNNINDQNNEYKLRIVKF	722	A; Molecule type: DNA A; Residues: 1-450 <UNK> A; Cross-references: UNIPROT:P38490; GB:Z99115; PID:92634723; PIC
Qy	144	-KENQQISYKDLEN-----NVGSVLSKSNR-----GTDV-----DLRSKDKAF	181	A; Experimental source: strain 168 R; Moriyama, R.; Hattori, A.; Miyata, S.; Kudoh, S.; Makino, S.
Db	723	ENKPEPSYLYKNTINNDWDNIFYDTNKGSVVIKSNTSNTSYAGIVDITNDHNIYTNTNTSY	782	J. Bacteriol. 178, 6059-6063, 1996
Qy	182	T-YNFKNSTKVKI 193	193	A; Title: A gene (<i>splyB</i>) encoding a spore cortex-lytic enzyme from <i>Bacillus subtilis</i> and a reference number: Z22836; MUID:96427343; PMID:8830707
Db	783	TYVSFGSYRKLI 795	795	A; Accession: T4471 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-331 <MOR> A; Cross-references: EMBL:D79978; PID:91688021; PIDN:BA11474.1; PID:g1688024 A; Experimental source: strain 168 C; Genetics:
RESULT A3856				
surface-layer 125k protein precursor - <i>Bacillus sphaericus</i>				
C; Species: <i>Bacillus sphaericus</i>				
C; ID: 09-Mar-1990 #sequence_change 09-Mar-1990 #text_change 09-Jul-2004				
C; Accession: A33056				
R; Bowditch, R.D.; Baumann, P.; Yousten, A.A.				
J; Bacteriol. 171, 4178-4188, 1989				
A; Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer protein				
A; Reference number: A33856; MUID:89327128; PMID:2663389				
A; Accession: A33056				
A; Status: Preliminary				
A; Molecule type: DNA				
A; Residues: 1-1176 <BOW>				
A; Cross-references: UNIPROT:P38537; GB:M283361; PID:9341911; PIDN:AAA50256.1; PID:9556012				
F; 93-147/Domain: S-layer repeat homology <SLR2>				
Query Match 20 VNGTSONQNLSSLTENKNCQISYKDIENKVKSNTYLFNRGQISDID-----LRLSKQAKY				
Best Local Similarity 22.4% Pred. No. 55/ Matches 44; Conservative 33; Mismatches 80; Indels 39; Gaps 7;				
Qy	20	VNGTSONQNLSSLTENKNCQISYKDIENKVKSNTYLFNRGQISDID-----LRLSKQAKY	72	Db 144 NELRHVQHLVMSKNLWMDVEMALASDEKQSDNTLINSFKTVKEVNGAFASTGTDLGFSFT 203
Db	176	IKGSEANCKTNL-NPNAPIRQDF-----AVVFSTTENVDAFPKVDKLEVVDAKTLN	227	Db 84 HNSVSQLPLTMFBNTBELISKIGDFSYKTSVRDLQKPLDKNBTSLNLKYQOQSDDIQ 143
Qy	73	VHFKNNGTRVVLDLKRAGITHADLINTSDKAISVNNDTKVQKDKEAKANVQPYTT-----129	129	Db 46 NKVKSVLYF---NRGTSIDIDLRS---KQAKYTV--HFKNGTKRVVDLKGIAHTADLIN 96
Db	228	VTLSQDGTVKETVLE-----KALEBNKETEVTFKIKDVEYKAKTVVTTAT 273	273	Db 144 NELRHVQHLVMSKNLWMDVEMALASDEKQSDNTLINSFKTVKEVNGAFASTGTDLGFSFT 203
Qy	130	-VNGTSONQNLSSLTENKNCQISYKDIENKVKSNTYLFNRGQISDIDRLU-SKOAKFTVNFKN	187	Db 84 HNSVSQLPLTMFBNTBELISKIGDFSYKTSVRDLQKPLDKNBTSLNLKYQOQSDDIQ 143
Db	274	AVKSVSATNLKEVVFEGTVDEKTAEDAAANTALKSGRTKTSVSLAADNKTATVTLTDKL	333	Db 97 T-----SDTAKAISVNVDTPKQKDVQKDKEA-----KANVQPYTTVNTGTS 134
Qy	188	GTVKK---VIDLKAG 198	198	Db 204 STIKKEEKGPFSHLKGKQISEQAKQIAERFAPPDNYSIKVVKSGKTKNRDV-YISISMKDPD 262
Db	334	NNNKADAIISVNKVAG 349	349	Db 144 NELRHVQHLVMSKNLWMDVEMALASDEKQSDNTLINSFKTVKEVNGAFASTGTDLGFSFT 203
RESULT E69934				
conserved hypothetical protein ypeB - <i>Bacillus subtilis</i>				
C; ID: 05-Dec-1997 #sequence_change 05-Dec-1997 #text_change 09-Jul-2004				
C; Accession: E69934; T4471				
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Aloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodat, J.; Erlich, S.D.; Emmerling, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Harwood, C.R.; Hensau, A.; Hilbert, H.; Hollsappel, S.; Hobono, S.; Hull, M.F.; Koettler, P.; Koningsrein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapius, A.; Lardinois, A.; Authors Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Matsuda, S.; Maezel, Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteelle, Rieger, M.; Rivolta, C.; Rocha, E.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors Schleicher, S.; Schroeter, R.; Sofrone, P.; Sekiguchi, J.; Sekiwaka, A.; Seror, Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Togoni, A.; Totato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors Yoshihikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.				
A; Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . A; Reference number: A69580; MUID:98044033; PMID:9384377				
A; Accession: E69934				
A; Status: preliminary; nucleic acid sequence not shown; translation not shown				
RESULT 28				
conserved hypothetical protein ypeB - <i>Bacillus subtilis</i>				
C; ID: 05-Dec-1997 #sequence_change 05-Dec-1997 #text_change 09-Jul-2004				
C; Accession: E69934				
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Aloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodat, J.; Erlich, S.D.; Emmerling, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Harwood, C.R.; Hensau, A.; Hilbert, H.; Hollsappel, S.; Hobono, S.; Hull, M.F.; Koettler, P.; Koningsrein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapius, A.; Lardinois, A.; Authors Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Matsuda, S.; Maezel, Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteelle, Rieger, M.; Rivolta, C.; Rocha, E.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors Schleicher, S.; Schroeter, R.; Sofrone, P.; Sekiguchi, J.; Sekiwaka, A.; Seror, Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Togoni, A.; Totato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors Yoshihikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.				
A; Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . A; Reference number: A69580; MUID:98044033; PMID:9384377				
A; Accession: E69934				
A; Status: preliminary; nucleic acid sequence not shown; translation not shown				
RESULT 47				
KVKSVLYFNRGTSIDDLRSQAKYTVHFK-NGTTRVVDLK-----46				
Qy	90	SHAHADHTGMVGLIDEKIPLMLMTGGETFAVMRASVTSNSVNLQGGKRRKVNDLLEN	149	Db 90 SHAHDHTGMVGLIDEKIPLMLMTGGETFAVMRASVTSNSVNLQGGKRRKVNDLLEN
Qy	90	VNGTSONQNLSSLTENKNCQISYKDIENKVKSNTYLFNRGQISDIDRLSQAKYTVHFK-NGTTRVVDLK-----46	149	Db 90 VNGTSONQNLSSLTENKNCQISYKDIENKVKSNTYLFNRGQISDIDRLSQAKYTVHFK-NGTTRVVDLK-----46

Db	150 GIREDTVSPONSKNAEKGTRRVSPKNTIENNDLTIVDVSILWNKNELLFVEPVYHVSIGA	209	Qy	21 NGTSQNILLSLTENKNQOISYKDIENKVSKVSVLYFNRGT-----SDIDLRLSKOAKYTGVHF	75
Qy	87 AGI-----HTADL-----INTSDIKAI5SYNDTKK---QVKDKEAKA	120	Db	331 NGNLDIFVLSFLPKSN-TLPISLQSIRSSL--LLAFRSNNINTWSEITELLYDGRYCQEP	387
Db	210 AGLAARVDIWLAYTCDFRTGPETABEERYWDLTGKEIRLALSRTSRPENLKDRLR---	266	Qy	76 KNGTKRVDLKGAGHTADLINTSDIKAI5SYNDTKVOKDKEAKANVQPYTTITVNGTSQ	135
Qy	121 NVQVPYITTINGTSQNLISNLTEPKNQOISYKDLENNNSVYLSKNSRGITDWD	172	Db	388 RGPTPEAV-----GNFLYNLIDMSDSEVQAEERHLRQEMLNKVLPENI-YRG1-R	440
Db	267 -----PLVYLVEGT-----RVTREENIENTEKDVPEANAVVERGTVNLIVD	308	Qy	136 NIL-----SNTLFKNQOISYKDLENNNSVYLSKNSRGITDWDRLSK	177
			Db	441 NLLESYHYPPELIKDAHLLVERKNULDFOQTIVQLTSSESTLETIKAENQPIRDY---LK	496
RESULT 30			Qy	178 QAKFTVNFKNGTKKVIDKA	197
A66873 transcription regulator yugA [Imported] - Lactococcus lactis subsp. lactis			Db	497 QLIVLVCSEENMQRKALELKA	516
C; Species: Lactococcus lactis subsp. lactis ^B					
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004					
C; Accession: A66873					
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaiion, O.; Malarrie, K.; Weissenbach, J.; Ehrlich, K.; Genome Res.	11, 731-753, 2001				
A; Reference number: A66873; MUID:21235186; PMID:11337471					
A; Accession: A66873					
A; Status: preliminary					
A; Molecule type: DNA					
A; Residues: 1-244 <STO>					
A; Cross-references: UNIPROT:Q9ZB19; GB:AE005176; PID:912725030; PIDN:AAK06083_1; GSPPDB:G					
A; Experimental source: strain IL1403					
C; Genetics:					
A; Gene: yugA.					
Query Match	9.6%	Score 97.5; DB 2; Length 244;			
Best Local Similarity	22.3%	Pred. No. 9.4; Indels 69; Gaps 8;			
Matches 44; Conservative 30; Mismatches 49; Indels 69; Gaps 8;					
Qy	20 VNGTSQNILLSLTENKNQOISYKDIEN-----KVKSVLYFNRGIS-----D 60				
Db	68 INGSKEVTLGATA--KNOQEELKTIENSAEIEKAVELIQESEETLIFSRGLSTNVADE	125			
Qy	61 IDTRLR-----SKQAKTYVHPKNGTKRVDLKGAGHTADLINTSDIKAI5SYND	108			
Db	126 LMKKQLQFLRKPKVSLHDSSKYMAYYARFVNEKSLIVLSSGETVELNALN-----	177			
Qy	109 TKGQVKDPEANAVQPYTTITN-GTSQNLISNLTEPKNQOISYKDLENNNSVYLSK	164			
Db	178 -----AKGONPKTSLTVNANTSLTNLSDISLGKSSLEVNYPDL-----	218			
Qy	165 NRGITDWDRLS 176				
Db	21.9 -----DVSRLS 225				
RESULTS 31					
S27954 Leucine-rich protein - human					
C; Species: Homo sapiens (man)					
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999					
C; Accession: S27954					
R; Hou, J.; Wang, F.; Adams, P.; McKesson, W.L.					
Submitted to the EMBL Data Library, May 1992					
A; Description: A novel 130 kd leucine rich protein.					
A; Reference number: S27954					
A; Accession: S27954					
A; Molecule type: mRNA					
A; Residues: 1-1207 <HOU>					
A; Cross-references: ENBL:MG24349; NID:9177109; PIDN:AAA67550_1; PID:9177110					
C; Genetics:					
A; Gene: GDB:HILRP					
A; Cross-references: GRB:455175					
Query Match	9.6%	Score 97.5; DB 2; Length 1207;			
Best Local Similarity	24.0%	Pred. No. 66; Indels 79; Gaps 8;			
Matches 48; Conservative 36; Mismatches 36; Indels 37; Gaps 8;					

A;Cross-references: UNIPROT:Q99053; GB:BA000018; PID:g13701233; PID:BA042528.1; GSPDB:G
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: ebbN

Query Match 9.5%; Score 97; DB 2; Length 3890;
 Best Local Similarity 21.4%; Pred. No. 3e-02; Mismatches 31; Indels 76; Gaps 9;
 Matches 49; Conservative 31; Mismatches 73; Indels 76; Gaps 9;

Qy 17 TITVNGTSONILSNTPKRNQISYKTFENKVSKVLYTNRG--ISDIDLRLRSQAKYTVH 74
 Db 1036 TAVSNDEQSIITAP-MNKGQN1-----RGYLASTDVTVDNNGNVTLH 1078

Qy 75 PKNGTKRVD-----LKAIGIHTADLINTSDI--KAISVNVDTCKQVTDKEAKAN 121
 Db 1019 YRGSSSTLDATNVMTYBPPVRSBYQTAAKATATVIAKGGSFNTGIDIKQY----- 1130

Qy 122 VQVPTYT-----VNGTISONILSNTPKRNQISYKTFENKVSKVLSNR----- 166
 Db 1131 ----FVLSNGQAIPTNNTSDRTIQAQEVSONNAGTOLYHIVASNAVYHDKTEDFYI 1186

Qy 167 --GITDV-----DLRSLRSQAKFTVNFKNFGTRKVIDLKG 198
 Db 1187 SLKIVDVKQPEQGDQRYVFTSTYDLTDBISKVQAFAINANRDVITLAEG 1235

RESULT 34
 AC1098 B. subtilis YabE protein homolog lmo0186 [Imported] - Listeria monocytogenes (strain EGDe)
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AC1098
 R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fehl, H.; Jones, L.M.; Kars, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varoqueix-Boland, J.A.; Voss, H.; Weiland, A.; Reference number: AB1077; PMID:21537279; PMID:11679669
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varoqueix-Boland, J.A.; Voss, H.; Weiland, A.; Reference number: AB1077; PMID:21537279; PMID:11679669
 A;Title: Comparative genomics of Listeria species.
 A;Accession: AC1098
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-408 <GLA>
 A;Cross-references: UNIPROT:Q8YAB4; GB:NC_003210; PID:GAC98401.1; PID:g16409543; GSPDB:
 A;Experimental source: strain Egde-e
 C;Genetics:
 A;Gene: lmo0186

Query Match 9.5%; Score 96.5%; DB 2; Length 408;
 Best Local Similarity 24.2%; Pred. No. 21; Mismatches 34; Indels 49; Gaps 10;
 Matches 50; Conservative 34; Mismatches 74; Indels 49; Gaps 10;

Qy 11 GSQIPIY-----TITVNGTSONILSNTPKRNQISYKTFENKVSKVLYTNRG----- 52
 Db 89 GMBIKYLPARQITINDNTKDWSTRKANVADLKDENTITTPQDVNLVALPTKLNGLE 148

Qy 53 -YPNRGISDIDLRLRSQAKFTVNFKNFGTRKVIDLKGAGIHTADLINTSDIKAISVNVDTCK 111
 Db 149 VNINRAI-----QLSLQ-----NGRKKDVTWTTKVKVSDILAERKIK-----LDQDD 190

Qy 1112 QV---KDEAKAKANQVQPTYTITYNGTSONILSNTPKRNQISYKTFENKVSKVLSNRGI 168
 Db 191 RVSPAKDSNLKEMTIVTY-JNSKAE-----KREQVKPFETVKEEDSLNKGVFRV 241

Qy 169 TDVDRLSRSQAKFTVNFKNFGTRKVIDL 195
 Db 242 VQEKGNGKXKVEYKVFENGKEKRDV 268

RESULT 35
 G97827 hypothetical protein RC1023 [Imported] - Rickettsia conorii (strain Malish 7)

Db 109 -----TICKYOKDKE-----AKANQVPTYI----- 108
 Db 107 RLKNEKGEBWLFLYKTRKKQENTESLIPKITESALKNIKISMRWWGDQNQKFSPRIRNIVI 166

Query Match Score 9.4%; DB 2; Length 377;
 Best Local Similarity 24.3%; Pred. No. 22; Gaps 12;
 Matches 54; Conservative 30; Missmatches 63; Indels 12;

Query Match Score 95.5%; DB 2; Length 377;
 Best Local Similarity 21.4%; Pred. No. 35; Gaps 10;
 Matches 52; Conservative 35; Missmatches 77; Indels 79; Gaps 10;

RESULT 37
 H82882 hypothetical protein UU497 [imported] - Ureaplasma urealyticum
 C; Species: Ureaplasma urealyticum
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C; Accession: H82882
 R; Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor reference sequence number: A82870
 A; Reference number: H82882
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-377 <GLA>
 A; Cross-references: GB:AE002148; GB:AF222894; NID:96899495; PIDN:AAF30909.1; GSPDB:GN001
 A; Experimental source: serovar 3; biovar 1
 C; Genetics:

A; Gene: UU497
 A; Genetic code: SGC3

Query Match Score 9.4%; DB 2; Length 377;
 Best Local Similarity 21.4%; Pred. No. 35; Gaps 10;
 Matches 52; Conservative 35; Missmatches 77; Indels 79; Gaps 10;

Query Match Score 95.5%; DB 2; Length 682;
 Best Local Similarity 20.5%; Pred. No. 45; Gaps 12;
 Matches 54; Conservative 39; Missmatches 55; Indels 115; Gaps 12;

RESULT 39
 F90603 valve-like (mycoplasma hyorhinis) lipoprotein [imported] - Mycoplasma pulmonis (strain UA
 C; Species: Mycoplasma pulmonis
 C; Accession: F90603
 R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Mooser, I.;
 Nucleic Acids Res., 29, 2145-2153, 2001
 A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmo
 A; Reference number: A99512; MUID:21267165; PMID:11353084
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-682
 A; Cross-references: UNIPROT:Q98P18; GB:AL445566; PIDN:914090149; PIDN:CA13907.1; GSPDB:G
 A; Experimental source: strain UAB CTIP
 A; Gene: MTPU_7340
 A; Genetic code: SGCC3

Query Match Score 9.4%; DB 2; Length 682;
 Best Local Similarity 20.5%; Pred. No. 45; Gaps 12;
 Matches 54; Conservative 39; Missmatches 55; Indels 115; Gaps 12;

Query Match Score 95.5%; DB 2; Length 682;
 Best Local Similarity 20.5%; Pred. No. 45; Gaps 12;
 Matches 54; Conservative 39; Missmatches 55; Indels 115; Gaps 12;

RESULT 40
 C97183 probable nucleotidyltransferase [imported] - Clostridium acetobutylicum
 C; Species: Clostridium acetobutylicum

Search completed: March 16, 2005, 10:43:23

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RESULT 2
US-09-982-992A-2
; Sequence 2, Application US/09982992A
; Patent No. US20020164337A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M. et al.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE MAP PROTEIN AND METHOD OF USE IN TREATMENT
; FILE REFERENCE: P06522US02/BAS
; CURRENT APPLICATION NUMBER: US/09/982,992A
; CURRENT FILING DATE: 2001-10-22
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/241,832
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-982-992A-2

Query Match 61.6%; Score 626; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSHHHHHGSQIPTYTNGTSQNLSSLTENKVNQISYKDIEENKVSKVLYFNRGID 60
Db 1 MRGSHHHHHGSQIPTYTNGTSQNLSSLTENKVNQISYKDIEENKVSKVLYFNRGID 60

Qy 61 IDLRLSKQAKTYVHFKNGTKRVDLKGAIHTADLINTSDIKAI\$NVDTKQVKDKEAKA 120
Db 61 IDLRLSKQAKTYVHFKNGTKRVDLKGAIHTADLINTSDIKAI\$NVDTKQVKDKEAKA 120

Qy 121 NV 122
Db 121 NV 122

RESULT 4
US-08-781-986A-5238
; Sequence 5238, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunisch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEES: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSdos version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB2488DP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5238

Query Match 43.3%; Score 440; DB 8; Length 150;
Best Local Similarity 78.9%; Pred. No. 8.5e-27;
Matches 86; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 4 SHHHHHHGSQIPTYTNGTSQNLSSLTENKVNQISYKDIEENKVSKVLYFNRGID 63
Db 42 SLHRRyskvhvPvAATVNGTSQNLSSLTENKVNQISYKDIEENKVSKVLYFNRGID 63

Qy 64 RLSKQAKTYVHFKNGTKRVDLKGAIHTADLINTSDIKAI\$NVDTKKKQ 112
Db 102 RLSKQAKTYVHFKNGTKRVDLKGAIHTADLINTSEIKAININTDKKKQ 150

RESULT 3
US-10-041-775-4
; Sequence 4, Application US/10041775
; Publication No. US20030108564A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, Eric L.
; APPLICANT: LIFE, Lawrence
; APPLICANT: HOOK, Magnus
; TITLE OF INVENTION: METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF THE TITLE OF INVENTION: HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN)
; FILE REFERENCE: P01023US01/BAS
; CURRENT APPLICATION NUMBER: US/10/041,775
; CURRENT FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2001-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-041-775-4

RESULT 5
US-10-329-624-5238
Sequence 5238, Application US/10329624

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-DEC-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5238:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-10-329-624-5233

Query Match 43.3%; Score 440; DB 15; Length 150;
Best Local Similarity 78.9%; Pred. No. 8.5e-27;
Matches 86; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
Qy 4 SHHHHHGSOIPTYTIVNGTSNQLSSLTENKVNQISYKDILENKVSVLYFNRGTSIDDI
Db 42 SLHGGTSKVHYAITYTNGTSNQLSSLTENKVNQISYKDILEDRVKSLKSDRGSDIDL 101
Qy 64 RLSKQAKYTVAHKNGTKRVDLKGAGHTADLINTSDIKAIISVNVDTKQ 112
Db 102 RLSKQAKYTVAHKNGTKRVDLKGAGTYADLINTSEIKAININVDTKQ 150

RESULT 6
US-08-781-986A-5233

Sequence 5233, Application US/10329624

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*
NUMBER OF SEQUENCES: 5255

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*
NUMBER OF SEQUENCES: 5255

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/329,624
 FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/956,171
 FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman

REGISTRATION/DOCKET NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248PLD1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8339

INFORMATION FOR SEQ ID NO: 5233:

SEQUENCE CHARACTERISTICS:
 LENGTH: 151 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 5233:

US-10-329-624-5233

Query Match 20.7%; Score 210; DB 15; Length 151;
 Best Local Similarity 44.3%; Pred. No. 7.1e-39;
 Matches 43; Conservative 22; Mismatches 0;
 Indels 0; Gaps 0;

Qy 14 I P Y T I V N G T Q S N I L S S T F N R Q Q I S Y K D I E N K V S Y L V F N R Q I S D I D I R L S K Q A K Y T V 73
 Db 55 V P Y T I A D G I M A F N Q S Y L N P K D S Q I S Y D I G N Y K V A L L I D E R G T P E K R N A K S A V Y T I 114

Qy 74 H F K N G T K R V D L K A G I H T A D I N T S D I K A I S V N V D T K 110
 Db 115 T W K D G S K R E V D L K D S T A N L F D S N S I K Q I D I N V K T K 151

RESULT 8
 US-10-470-048B-221
 Sequence 21, Application US/10470048B
 Publication No. US/05003744A1

GENERAL INFORMATION:
 APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF ANTIGENS TO A SPECIFIC PATHOGEN

FILE REFERENCE: SONN:035US

CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603
 SEQ ID NO: 221
 LENGTH: 141

ORGANISM: Staphylococcus aureus

US-10-470-048B-221

Query Match 14.0%; Score 142; DB 17; Length 141;
 Best Local Similarity 33.0%; Pred. No. 0.0013;
 Matches 31; Conservative 25; Mismatches 38;
 Indels 0; Gaps 0;

Qy 14 I P Y T I V N G T Q S N I L S S T F N R Q Q I S Y K D I E N K V S Y L V F N R Q I S D I D I R L S K Q A K Y T V 73
 Db 47 V P Y T I S G I T A L H R T F I P E K N A V L Q E I D S K V N E L A S O R G V T E K I N N A Q T A T Y T L 106

Qy 74 H F K N G T K R V D L K A G I H T A D I N T S D I K A I S V N V D T K 107
 Db 107 T W L D G N K K V V N L K C N D D A R N S I D P S T I K Q I Q I V V 140

RESULT 9

US-10-378-674-4
 Sequence 4, Application US/10378674

GENERAL INFORMATION:
 APPLICANT: PATTI, Joseph M.

TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI

TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS

FILE REFERENCE: P07556US01/BAS

CURRENT APPLICATION NUMBER: US/10/378,674

CURRENT FILING DATE: 2003-03-05
 PRIORITY APPLICATION NUMBER: 60/361,324

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 4

LENGTH: 343

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-10-378-674-4

Query Match 13.1%; Score 133; DB 15; Length 343;

Best Local Similarity 22.4%; Pred. No. 0.02;
 Matches 54; Conservative 32; Mismatches 71;
 Indels 84; Gaps 9;

Qy 1 M R G S H H H H H G S Q I P ----- Y T I V N G T Q S N I L S S T F N I S D I U T K V D Q S I T E G Y D D S G I T K A H D A E N L Y D V T F 60

Db 1 M R G S H H H H H G S L V E R G S B O G S N V N H L I K V T D Q S I T E G Y D D S G I T K A H D A E N L Y D V T F 60

Query Match 12.9%; Score 131; DB 15; Length 316;

Best Local Similarity 22.6%; Pred. No. 0.025;
 Matches 53; Conservative 33; Mismatches 71;
 Indels 78; Gaps 9;

Qy 1 M R G S H H H H H G S Q ----- I P Y T I V N G T Q S N I L S S T F N I S D I U T K V D Q S I T E G Y D D S G I T K A H D A E N L Y D V T F 39

Db 1 M R G S H H H H H G S L Q E Q G S N V N H L I K V T D Q S I T E G Y D D S G I T K A H D A E N L Y D V T F 54

RESULT 11
 US-10-057-531A-7
 Sequence 7, Application US/10057531A
 Publication No. US20030161839A1
 GENERAL INFORMATION:
 APPLICANT: Lyon, Jeffrey A.
 APPLICANT: Angov, Evelina
 TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite
 FILE REFERENCE: 003/241/SAP
 CURRENT FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: US 60/264,535
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: US 60/347,564
 PRIOR FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ ID NO 7
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)
 US-10-057-532A-7

Query Match 11.4%; Score 117.5; DB 14; Length 391;
 Best Local Similarity 22.2%; Pred. No. 0.37; Mismatches 91; Indels 57; Gaps 9;
 Matches 52; Conservative 34; Mismatches 91; Indels 57; Gaps 9;

Qy 4 SHHHHHH-GSQIPYTTVNGTSONISSLTPNKNQISY-----KDIENKVKS 50
 Db 2 AHHHHHHPGGSGSGTMAISVTMDNLSG--FENEVDVYLPLAGYRSLRKQIE--KN 56
 Qy 51 VLYFNRGISDDLRLSKOAKYTVAHFKRVLKAGIHTPADLNTSDIKAIISVNVDTK 110
 Db 57 IFTENNLNDLINSRLKCKYFL-----DVLESDLQFKHISSENEYIEDS 102
 Qy 111 KQVKDKBAAKANQVPYTTVNGTSONI---LSNLTPKFKNQISYKDLENVYKSVLNSR- 166
 Db 103 FKLLNSEQNTLKLSKYKIESVENDIKPAOBGISTYEKVLAKYKDLESIKVKEKB 162
 Qy 167 -----GTTDVDRLSKQAKFTVW--FKNGTKV----IDIKAGI 199
 Db 163 KFPSSPPTPPSPAKTDEQKESKLPFLTNIETLYNNLYNKIDDYLNLKAKI 216

RESULT 12
 US-10-057-532A-7
 Sequence 7, Application US/10057532A
 Publication No. US20030161839A1
 GENERAL INFORMATION:
 APPLICANT: Lyon, Jeffrey A.
 APPLICANT: Angov, Evelina
 APPLICANT: Cohen, Joe D.
 APPLICANT: Voss, Gerald
 TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine
 FILE REFERENCE: 003/238/SAP
 CURRENT APPLICATION NUMBER: US/10/057,532A

CURRENT FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: US 60/264,535
 PRIOR FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 12
 SEQ ID NO 7
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)

Query Match 11.4%; Score 117.5; DB 14; Length 391;
 Best Local Similarity 22.2%; Pred. No. 0.37; Mismatches 91; Indels 57; Gaps 9;
 Matches 52; Conservative 34; Mismatches 91; Indels 57; Gaps 9;

Qy 4 SHHHHHH-GSQIPYTTVNGTSONISSLTPNKNQISY-----KDIENKVKS 50
 Db 2 AHHHHHHPGGSGSGTMAISVTMDNLSG--FENEVDVYLPLAGYRSLRKQIE--KN 56
 Qy 51 VLYFNRGISDDLRLSKOAKYTVAHFKRVLKAGIHTPADLNTSDIKAIISVNVDTK 110
 Db 57 IFTENNLNDLINSRLKCKYFL-----DVLESDLQFKHISSENEYIEDS 102
 Qy 111 KQVKDKBAAKANQVPYTTVNGTSONI---LSNLTPKFKNQISYKDLENVYKSVLNSR- 166
 Db 103 FKLLNSEQNTLKLSKYKIESVENDIKPAOBGISTYEKVLAKYKDLESIKVKEKB 162
 Qy 167 -----GTTDVDRLSKQAKFTVW--FKNGTKV----IDIKAGI 199
 Db 163 KFPSSPPTPPSPAKTDEQKESKLPFLTNIETLYNNLYNKIDDYLNLKAKI 216

RESULT 13
 US-09-813-820-6
 Sequence 6, Application US/09813820
 Patent No. US2002010222A1
 GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Patti, Joseph M.
 House-Pompeo, Karen
 Sthanam, Narayana
 Symarsky, Jindrich
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.
 ZIP: 77210
 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.1.30
 APPLICATION NUMBER: US/09/813,820
 FILING DATE: 22-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/856,253
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: TAMK,193
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 512 amino acids
 TYPE: amino acid
 STRANDNESS: <Unknown>
 TOPOLOGY: linear
 SEQ ID NO: 6:
 US-09-813-820-6

Query Match 11.5%; Score 116.5; DB 9; Length 512;
 Best Local Similarity 23.8%; Pred. No. 0.63; Gaps 14;
 Matches 64; Conservative 29; Mismatches 79; Indels 97; Gaps 13;

Qy 1 MRGSHHHHHGSGQIPTTYTNGTSNLISS-----LTF-NRNQQTSYKD---- 43
 Db 1 MRGSHHHHHGSGARDISST-NVTDLTSPSKIEDGGKTTVRMTEDKGKTIQONGMIVKA 59
 Qy 44 -----IENKVKS-----LYFN---RGISDIDLRLSKOAKYT 72
 Db 60 WPTSGTYKVEGSKTVPLTVRGQAVIPDGATITFNDKEVLSDV---SGFAEFE 115
 Qy 73 VHFNGTKRVDLKGAGHTADLINTSDIKAI SV--NVDTKQVKDKEA----- 118
 Db 116 VQGRNLQT-----TNTSDDKVATITSGNKSTNVTHKSEACTSSVFYKTG 161
 Qy 119 ---KANVQVPYTITNGTSNLISSNLFK-----NQQISYKDLENN----- 166
 Db 162 DMLPEDTHVRMFLNINNEKSYSDKIDTIDQIGQQLDLSLTNINTGTHSNYYSGQS 221
 Qy 167 GITDVDLRLSKOAKFTNFKRNGTKVVDLKGAY 195
 Db 222 AITDFE-KAFPGSKITV--DNTKNTIDV 246

RESULT 14
 US-10-282-122A-72043
 Sequence 72043, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION
 APPLICANT: Wang, Li angsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Porscht, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: EILTRA-034A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-16
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-04-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 72043
 LENGTH: 374
 TYPE: PRT
 ORGANISM: Streptococcus mutans
 US-10-282-122A-72043

Query Match 11.3%; Score 115; DB 15; Length 374;
 Best Local Similarity 24.2%; Pred. No. 0.55; Gaps 13;
 Matches 52; Conservative 42; Mismatches 63; Indels 58; Gaps 13;

Qy 18 ITVNNGTSONLISSTFNKNQOISYKDIENKVKSVL-----FNRGISDIDLRLSKOAKYT 73
 Db 131 ITVSNKNAESQJL-----BEGIJKK-SDYLTLTLFQANRFERNLKSKD-KWVKHAKLV 184
 Db 74 HFNGK-TKRVFD-----LKAGIHTADLINTSDIKA-1SVNNDTQDKQV 114
 Db 185 HFPNHFETLKEYRLLAYRQTDK3GYVPLLENGTR-VDTVNASELPSFTVNLQEQEVK 243
 Qy 115 -----DREAKANVQPVYPTITNGTSNLLSNLTFKKNNQOISYKDLENNVSVLKSN 165
 Db 244 ELVQCLAKLDKLSVLSVIKV--ISSNNSSTKDLLEMDN-----NSVRVPL--- 289

Db 166 RGITDVDLRLSKOAKFTNFKRNGTKVVDLKGAY 200
 Qy 290 ---SEIDTKLPYSSKIKNLTDGS--IVDMEVGTY 319

RESULT 15
 US-10-057-531A-3
 Sequence 3, Application US/10057531A
 Publication No. US20030161838A1
 GENERAL INFORMATION:
 APPLICANT: Lyon, Jeffrey A.
 APPLICANT: Angov, Evelina
 TITLE OF INVENTION: Isolation and Purification of *P. falciparum* Merozoite
 TITLE OF INVENTION: Protein-142 Vaccine
 FILE REFERENCE: 003/241/SAP
 CURRENT APPLICATION NUMBER: US/10/057,531A
 CURRENT FILING DATE: 2003-01-25
 PRIOR APPLICATION NUMBER: US 60/264,535
 PRIOR FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: US 60/347,564
 PRIOR FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ ID NO: 3
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Sequence in PERT2A
 US-10-057-531A-3

Query Match 11.3%; Score 114.5; DB 14; Length 393;
 Best Local Similarity 22.5%; Pred. No. 0.64; Gaps 10;
 Matches 53; Conservative 34; Mismatches 90; Indels 59; Gaps 10;

Qy 4 SHHHHH-GSQ1P-YTITYVNGTSNLLSNLTFKKNNQOISY-----KJENKV 48
 Db 2 AHHHHHPGGSIEGRGTMASVTMDNLSG-FENEBDVYLLKPLAGVYRSLKQKQE--- 56

Qy 49 KSVLVYNGRGSIDIDLRLSKOAKYTFRKQNETKRVYDVLKAGHTADLINTSDIKASVND 108
 Db 57 KNIFTFNLNLDLNLNLSRLKGRKFPL-----DYLESDLMOFRKHISSENEYIE 102

Qy 109 TKQQVKDKEAKANVQVPYTITNGTSONI---LSNLTFKRNQISYKDLENNVSVLKSN 165
 Db 103 DSFKLNLSEQRNLTLLKSYKIKESVENDIKFAQEGISYERKLYKTDLESIKVKEE 162
 Qy 166 R-----GITDVDLRLSKQAKFTYN---FNGTCKV---IDLKAGI 199
 Db 163 KEKFPSSPPTPPSPAKTDEQKKESELFLNLTETLYNNLVNKIDDYLINLKAKI 218

RESULT 16
 US-10-057-532A-3
 Sequence 3, Application US/10057532A
 Publication No. US2003016183941
 GENERAL INFORMATION
 APPLICANT: Lyon, Jeffrey A.
 APPLICANT: Angov, Evelina
 APPLICANT: Cohen, Joe D.
 APPLICANT: Voss, Gerald
 TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine
 FILE REFERENCE: 003/238/SAP
 CURRENT APPLICATION NUMBER: US/10/057,532A
 CURRENT FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: US 60/264,535
 PRIOR FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: US 60/347,564
 PRIOR FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ ID NO 3
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE: OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D) Protein Sequence in
 us-10-057-532A-3

Query Match 11.3%; Score 114.5; DB 14; Length 393;
 Best Local Similarity 22.5%; Pred. No. 0.64;
 Matches 53; Conservative 34; Mismatches 90; Indels 59; Gaps 10;

Qy 4 SHHHHH GSQIP---YTITVNGTSONISSLTENKRNQISY-----KDENKV 48
 Db 2 AHHHHHHEGGSTEGRGMASIVMDNISG--FENEVDVYKPLAGVYRSULKQLE--- 56

Qy 49 KSVLYENGIGSISDLRLSKQAKYTWFNGTCKRVDLKGAGIHTADINTDIKAI SVND 108
 Db 57 KNIFTFNHLNDLNSRKKYFL---DYLESDLMQKHISNEYIE 102

Qy 109 TKQQVKDKEAKANVQVPYTITNGTSONI---LSNLTFKRNQISYKDLENNVSVLKSN 165
 Db 103 DSFKLNLSEQRNLTLLKSYKIKESVENDIKFAQEGISYERKLYKTDLESIKVKEE 162

Qy 166 R-----GITDVDLRLSKQAKFTYN---FNGTCKV---IDLKAGI 199
 Db 163 KEKFPSSPPTPPSPAKTDEQKKESELFLNLTETLYNNLVNKIDDYLINLKAKI 218

RESULT 17
 US-09-813-820-4
 Sequence 4, Application US/09813820
 Patent No. US20020102262A1
 GENERAL INFORMATION
 APPLICANT: Hook, Magnus
 / Pacci, Joseph M.
 / House-Pompeo, Karen
 / Shaban, Narayana
 / Symersky, Jindrich
 / TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
 / AND METHODS OF USE
 / NUMBER OF SEQUENCES: 8
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Arnold, White & Durkee
 / STREET: P.O. Box 4433

CITY: Houston
 STATE: Texas
 COUNTRY: U.S.
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/813, 820
 FILING DATE: 22-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: 08/856,253
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: TAMK:193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 211 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-813-820-4

Query Match 11.2%; Score 114; DB 9; Length 211;
 Best Local Similarity 23.9%; Pred. No. 0.32;
 Matches 54; Conservative 28; Mismatches 84; Indels 60; Gaps 10;
 Qy 1 MRGSHHHHHHHSQIPYTITNGTSONISSLTENKRNQISYKDLENNVSVLKSN 60
 Db 1 MRGSHHHHHHHSDDKQVATISG-----NSTNVTVHKSEAGTSSVFYKTG--- 46

Qy 61 IDLRLSKQAKYTWFNGTCKRVDLKGAGIHTADINTS---DIKAISVNV---- 107
 Db 47 -DM-LPEDTHVRWPLNINNEKSYVSKDITIKDQLOGQQLDLSUNINVGTHSNVYSG 104

Qy 108 -----DTKQQVKDKEAKANVQVPYTITNGTSONILSNT----FKKNQO 148
 Db 105 QSAITDFEKAPPGSKLTVDNTKNTVTVTQGYGTSNSFSINYKTKITNEQQKEYFVNNSQ 164

Qy 149 ISYKD--LENNVSV----LKSNRGRTDV---DURLSKQAKFT 182
 Db 165 AWYQEHGKEEYNGKSFNHTVHNINAGIEGTVKGEKVLKQDKDT 210

RESULT 18
 US-10-282-122A-53616
 Sequence 53616, Application US/102822122A
 / GENERAL INFORMATION:
 / Publication No. US2004029129A1
 / GENERAL INFORMATION:
 / APPLICANT: Wang, Liangsu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cherry I
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohlsen, Kari
 / APPLICANT: Zybind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Forsyth, R.
 / APPLICANT: Xu, H.
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 / FILE REFERENCE: ELITRA.034A
 / CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20
 PRIORITY APPLICATION NUMBER: 60/191,078
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/205,848
 PRIORITY FILING DATE: 2000-05-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY FILING DATE: 2000-05-16
 PRIORITY APPLICATION NUMBER: 60/230,335
 PRIORITY FILING DATE: 2000-09-06
 PRIORITY APPLICATION NUMBER: 60/230,347
 PRIORITY FILING DATE: 2000-09-09
 PRIORITY APPLICATION NUMBER: 60/242,578
 PRIORITY FILING DATE: 2000-10-03
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-12-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/267,636
 PRIORITY FILING DATE: 2001-02-09
 PRIORITY APPLICATION NUMBER: 60/267,636
 PRIORITY FILING DATE: 2001-02-16
 PRIORITY APPLICATION NUMBER: 60/269,308
 PRIORITY FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 53616
 LENGTH: 246
 TYPE: PRT
 ORGANISM: Clostridium difficile
 US-10-282-122A-53616
 Query Match Score 11.2%; Best Local Similarity 22.0%; Pred. No. 0.43; Length 246;
 Matches 44; Conservative 40; Mismatches 65; Indels 51; Gaps 10;
 Qy 23 TSONQILSSLTENRQOI--SYDNIENKVKSYLYFURGISIDDLRSKQAKYTVPFRNGT 79
 Db 49 TKSNNIKELVNVLNENFAYNFEDMKNK---LIRNPYIENVEIRKLPNKKIIISIKE-- 102
 Qy 80 KRV-----VPLKAGIHTADLINTSDKA----ISVNVDTKQVKDKEAKANV 122
 Db 103 KEFAVLRKDENDNYCYIDRKGNI--LEELRGNSNSKDKLIVDVDSIDNNSIKFKNYK-- 158
 Qy 123 QVYPITITNGTQNQILSNTLTFKQNO---QISYKDL--ENNYSKVLKSNRGTIDVDRLLS 176
 Db 159 -----TKENVFTKLNVYIKEGYRKINVNLUKESNEMLTRSN---IKILS 203
 Qy 177 KQAKFTVNFQNGTKVKIDLK 196
 Db 204 NDDNLDDNISRVSKILDLQ 223
 RESULT 19
 US-10-282-122A-61097
 Sequence 61097, Application US/10282122A
 Publication No. US20040029123A1
 GENERAL INFORMATION
 APPLICANT: Wang, Liangshu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cherry
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zybskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsbych, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: EIJTRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-05-20
 PRIORITY APPLICATION NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-21
 ; PRIORITY APPLICATION NUMBER: 60/205,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-16
 ; PRIORITY APPLICATION NUMBER: 60/230,335
 ; PRIORITY FILING DATE: 2000-09-06
 ; PRIORITY APPLICATION NUMBER: 60/230,347
 ; PRIORITY FILING DATE: 2000-09-09
 ; PRIORITY APPLICATION NUMBER: 60/242,578
 ; PRIORITY FILING DATE: 2000-10-03
 ; PRIORITY APPLICATION NUMBER: 60/253,625
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: 60/267,636
 ; PRIORITY APPLICATION NUMBER: 60/269,308
 ; PRIORITY FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SEQ ID NO: 61097
 ; LENGTH: 963
 ; TYPE: PRT
 ; ORGANISM: Legionella pneumophila
 US-10-282-122A-61097
 Query Match Score 10.9%; Best Local Similarity 21.6%; Pred. No. 3.7; Matches 51; Conservative 46; Mismatches 73; Indels 66; Gaps 9;
 Qy 13 QVYPITITVN-GTSONQILSSLTENRQOISYKDLTENRVK---- 49
 Db 119 KIETTLTVNKKTEIATFLDLAQYQOLLNDVNLKLMKANPFDIKEKLKSIKAIKRL 178
 Qy 50 ----SVLYFNRGSIID----LRLSKQAKYTVPHFNGTKRVDLKGAIHTAD---- 93
 Db 179 NKLNLNLVY-AVSSDVKQPELTSEQIOEANYIYNORIAVHQKLNALELQKLIK 237
 Qy 94 ----LINTSDIKAIASVNDPTKKQVKDKEAKANVQVPTITYNGTQNQILSNTFCKN---- 146
 Db 238 TNLLLNLNLDTKALQSADINYNREVNQOYS----AIESSTQTLNSLNTQANLFV 287
 Qy 147 ---QQISYKDLIENNYKSVLKSNRGTIDVDRLLSKQAKFTVNFQNGTKVKIDLKAGI 199
 Db 288 EPGLOXKSVSLQNDVKTTELKET--SNOQLLISRNLE--DYQNLKKQISTROSL 337
 RESULT 20
 US-10-193-764-28
 Sequence 28, Application US/10193764
 Publication No. US20030133943A1
 GENERAL INFORMATION
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Yang, Yan Ping
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: PROTEIN RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
 FILE REFERENCE: 1038-1239WLS
 CURRENT APPLICATION NUMBER: US/10/193,764
 CURRENT FILING DATE: 2003-07-12
 PRIORITY APPLICATION NUMBER: 09/167,568
 NUMBER OF SEQ ID NOS: 91
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 28
 LENGTH: 1220
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-193-764-28
 Query Match Score 110; DB 14; Length 1220;

Best Local Similarity 23.7%; Pred. No. 6; Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

Qy 3 GSHHHHHGSQIPTYI-----TVNGTSQNII-SLTNKNQQISYKDIENKVKS 51
Db 422 GSDFDNH--QKPLTIKKDVIINSGNLTAGGVININGLNLYNGANL--KAITNFTFNV 476

Qy 52 --LYFNRCISIDDLRSKQAKYTVMFKTGTRVVDLKAGIHTADLINTSDIKAIISVNVT 109
Db 477 GGLFDNKGNSNTSI-----ARGAKPDRDNTSSIN-ITTNST 514

Qy 110 KQQ-----VKDEAKANVQVPTI-----TVNGTSQNII-SLTNLFKK-- 145
Db 515 TYRTTIEGNITNKAQDNLINIDNKGNATIQQIGENISQEGKNTTSDKINNITQITKKGV 574

Qy 146 NQOISYKDLLENNVSKVLSKQAKFTVNFNGTKRVT 193
Db 575 NKEDSDSSTANNANLTIKTKELQLTDLNIISGFDKAETAKEGADLII 622

RESULT 21
US-10-193-764-26
Sequence 26, Application US/10193764
Publication No. US2003033394A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michael H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
FILE REFERENCE: 103-8-1239MIS
CURRENT APPLICATION NUMBER: US/10/193,764
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 26
LENGTH: 1226
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-193-764-26

Query Match Score 110; DB 14; Length 1226;
Best Local Similarity 23.7%; Pred. No. 6; Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

Qy 3 GSHHHHHGSQIPTYI-----TVNGTSQNII-SLTNKNQQISYKDIENKVKS 51
Db 428 GSDFDNH--QKPLTIKKDVIINSGNLTAGGVININGLNLYNGANL--KAITNFTFNV 482

Qy 52 --LYFNRCISIDDLRSKQAKYTVMFKTGTRVVDLKAGIHTADLINTSDIKAIISVNVT 109
Db 483 GGLFDNKGNSNTSI-----ARGAKPDRDNTSSIN-ITTNST 520

Qy 110 KQQ-----VKDEAKANVQVPTI-----TVNGTSQNII-SLTNLFKK-- 145
Db 521 TYRTTIEGNITNKAQDNLINIDNKGNATIQQIGENISQEGKNTTSDKINNITQITKKGV 580

Qy 146 NQOISYKDLLENNVSKVLSKQAKFTVNFNGTKRVT 193
Db 581 NKEDSDSSTANNANLTIKTKELQLTDLNIISGFDKAETAKEGADLII 628

RESULT 22
US-10-041-667-5
Sequence 5, Application US/10404667
Publication No. US20040005332A1
GENERAL INFORMATION:
APPLICANT: Argov, Eyalina
APPLICANT: Lyon, Jeffrey A.
APPLICANT: Darko, Christian Asare
APPLICANT: Cohen, Joe D.

Best Local Similarity 23.7%; Pred. No. 6; Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

Qy 3 GSHHHHHGSQIPTYI-----TVNGTSQNII-SLTNKNQQISYKDIENKVKS 51
Db 422 GSDFDNH--QKPLTIKKDVIINSGNLTAGGVININGLNLYNGANL--KAITNFTFNV 476

Qy 52 --LYFNRCISIDDLRSKQAKYTVMFKTGTRVVDLKAGIHTADLINTSDIKAIISVNVT 109
Db 477 GGLFDNKGNSNTSI-----ARGAKPDRDNTSSIN-ITTNST 514

Qy 110 KQQ-----VKDEAKANVQVPTI-----TVNGTSQNII-SLTNLFKK-- 145
Db 515 TYRTTIEGNITNKAQDNLINIDNKGNATIQQIGENISQEGKNTTSDKINNITQITKKGV 574

Qy 146 NQOISYKDLLENNVSKVLSKQAKFTVNFNGTKRVT 193
Db 575 NKEDSDSSTANNANLTIKTKELQLTDLNIISGFDKAETAKEGADLII 622

Query Match Score 108.5; DB 15; Length 371;
Best Local Similarity 21.7%; Pred. No. 1-8; Matches 60; Conservative 39; Mismatches 79; Indels 99; Gaps 15;

Qy 4 SHHHHHH-GSQIPTYITVNGTSQNII-SLTNKNQQISYKDIENKVKS 50
Db 2 AHRRHHHPGGGSGGAVTPSVNDLISKI--ENEAEVLYKLPLAGYRSLSKKOLEN--N 56

Qy 51 VLYFNRCISID-LIRLSKQ-----AKYTV-----HPKNGTKRVVDLK 86
Db 57 VMTFENVVKDILNSRNKRENFKVNTLESIDLIPYKDLSITSSNVVKDIPYKFLNEKEKDKFLS 116

Qy 87 AGIHTADLINT-----SDIAKISVNVDTKQVKDKEAKANVQVPY 126
Db 117 SYNTKDSIDDINFANDVLGYKVULSEKYKSDLSI-----KCYINDKGENECKYLPF 170

Qy 127 TITVNGTSQNII-----ISNLNTPKK-NQOISYKDLLENNVSKV-----LKSN 165
Db 171 LNNIETLYKTVDNDKIDLFVHLEAVLNTYEKSNTEVKKTEL-NYLKTIQDKLADFKKN 229

Qy 166 R---GITDVDL-----RLSKOAKFTVNFNGTKRVT 193
Db 230 NNFVGIAIDLSTDYNHNLLTKPLSTGMVFENPAKTVL 266

RESULT 23
US-09-813-820-7
Sequence 7, Application US/09813820
Patent No. US20030102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
House-Pompeo, Karen
Sthanam, Narayana
SYMBRY, Jindrich
Address: Arnold, White & Durkee
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813.820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856, 253

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-813-820-7

Query Match 10.4%; Score 106; DB 9; Length 345;
Best Local Similarity 23.3%; Pred. No. 2.5;
Matches 52; Conservative 35; Mismatches 90; Indels 46; Gaps 11;

Qy 1 MRGSHHHHHGSQLPPTVNGTS-QNLISSLTENKVNQOIS-YKDIEKVKSVLYP--N 55
Db 1 MRGSHHHHHGSMVAADAPAGSTDITNQLNQTVGIDSGTIVYHQAGYTKLNYSFSVPN 60
Qy 56 RGSIDDLRSLSQAKYTVHFKNGTKRVDLKRAG-----IIFT-ADLINT-S 98
Db 61 SAVKGDTFKITVPKELNLNGTISTAKVPPIMAGDQVLANGYIDSGNVNIFTDVTNTKD 120
Qy 99 DIKAI-----SYNVDTRKQVKDKEAKANVQPV-----YTITVNGTSQNI 137
Db 121 DVKATLMPATIDPENYKTKGTNTLVTDYEKYGKFNLYNSIKGTIDQI 180
Qy 138 -LSNLTPKRNQOISYKDLENNPKVLSKNS-RGITDVDRLSKQ 178
Db 181 DKTNNTYRQTYVNPMSG-DVNTIAPVLTGIGSTANKTFLKENTDSNALIDQQ 222

RESULT 24
US-10-378-674-2
Sequence 2, Application US-10378674
Publication No. US2004006209A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M.
TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING CORTULASE-NEGATIVE ORGANISMS
FILE REFERENCE: P015560501.BAS
CURRENT APPLICATION NUMBER: US-10/378,674
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/361,324
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 560
TYPE: PRT
ORGANISM: *Staphylococcus epidermidis*
US-10-378-674-2

Query Match 10.3%; Score 105; DB 15; Length 560;
Best Local Similarity 24.6%; Pred. No. 5.5;
Matches 44; Conservative 18; Mismatches 41; Indels 76; Gaps 7;

Qy 1 MRGSHHHHHGSQLPPTVNGTSQNLISSLTENKVNQOISYKDVIEKVKSVLYFNGRS 58
Db 1 MRGSHHHHHGSSP-----ENTQYKDSNNDEL 29

Query Match 10.3%; Score 105; DB 15; Length 560;
Best Local Similarity 24.6%; Pred. No. 5.5;
Matches 44; Conservative 18; Mismatches 41; Indels 76; Gaps 7;

Qy 59 SDIDLRSLSQAKYTVHFKNGTKRVDLKRAGIHTADLINTSDIKASWVDTKKVKVDFKDEA 118
Db 30 SDSNDQSNEEK-----SINTDDENQIRKET 64

Query Match 10.3%; Score 105; DB 15; Length 560;
Best Local Similarity 24.6%; Pred. No. 5.5;
Matches 44; Conservative 18; Mismatches 41; Indels 76; Gaps 7;

Qy 119 KANVQV-----PYTITVNGTSQNLISSLTENKVNQOISYKDVIEKVKSVLYFNGRS 162
Db 68 TIKDQIQQGOODLSPLNINVGTGHSNYSGOSATIDFEKAPEGSKITVDNTKNTIDVTI 127

Query Match 10.2%; Score 104; DB 9; Length 159;
Best Local Similarity 20.6%; Pred. No. 1.4;
Matches 42; Conservative 29; Mismatches 53; Indels 80; Gaps 9;

Qy 1 MRGSHHHHHGSQLPPTVNGTSQNLISSLTENKVNQOISYKDVIEKVKSVLYFNGRS 60
Db 1 MRGSHHHHHGSSP-----TSNKSTNTVHK-----EGTSSSFYYK---- 38

Query Match 10.2%; Score 104; DB 9; Length 159;
Best Local Similarity 20.6%; Pred. No. 1.4;
Matches 42; Conservative 29; Mismatches 53; Indels 80; Gaps 9;

Qy 61 IDLRLSKQAKYTVHFKNGTKRVDLKRAGIHTADL-----NTSDIKASWVDTKKVKVDFKDEA 118
Db 39 -----TGDMLPEDTHVRWF-LNINNEKSIVSKDI 67

Query Match 10.2%; Score 104; DB 9; Length 159;
Best Local Similarity 20.6%; Pred. No. 1.4;
Matches 42; Conservative 29; Mismatches 53; Indels 80; Gaps 9;

Qy 119 KANVQV-----PYTITVNGTSQNLISSLTENKVNQOISYKDVIEKVKSVLYFNGRS 162
Db 68 TIKDQIQQGOODLSPLNINVGTGHSNYSGOSATIDFEKAPEGSKITVDNTKNTIDVTI 127

Query Match 10.2%; Score 104; DB 9; Length 159;
Best Local Similarity 20.6%; Pred. No. 1.4;
Matches 42; Conservative 29; Mismatches 53; Indels 80; Gaps 9;

Qy 163 KSNRGITDVLRSLSQAKYTVHFKNGTKRVDLKRAGIHTADLINTSDIKASWVDTKKVKVDFKDEA 118
Db 128 POGYG-----SYNSFSINYK 142

RESULT 26

US-10-282-122A-70558
 Sequence 70558, Application US/10282122A
 Publication No. US2004009129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangbu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Barry S.
 APPLICANT: Chen, Xianteng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10/52052/B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 4734
 SEQ ID NO: 2021
 LENGTH: 609
 TYPE: PRT
 ORGANISM: *Saccharomyces cerevisiae*
 US-10-369-493-2021

Query Match 10.2%; Score 103.5; DB 15; Length 609;
 Best Local Similarity 24.9%; Pred. No. 8;
 Matches 51; Conservative 29; Mismatches 56; Indels 69; Gaps 11;

Qy 24 SQN-TLSSLTENKNOISYKDI-EN-KVSVL-----YFNRGISDIDLRSKQAKYT 72
 Db 302 SONDKILKLETTNKAYTKYEVSLENKKIKBAFKELDNESYNH---DEBLLKCYKT 356
 Qy 73 VHFNGTKRVIDLKGAGHTADLINTSDIKASVNVDTKKQVKDEKEAN----- 121
 Db 357 ----- - RETLDRVNRQEQLIIDQNNEFLKKSYTELQEVNATNFKSULFE 400
 Qy 122 -VQVPTITNGTS---QNLISITFKNQQ---ISYKDLENNPKSVLKSNRGJTDV 171
 Db 401 KYAKLADSITELTNSTKREALEGENLFECNLKELBICLKYK--KNIENISNTNKLQN- 456
 Qy 172 DLRLSKOAKFTVNPKNGTKVKVIDLK 196
 Db 457 -----SFKNRKVYDILR 469

RESULT 28
 US-10-282-122A-60961
 Sequence 60961, Application US/10282122A
 Publication No. US2004009129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Forbych, R.
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELTRA 034A
 CURRENT APPLICATION NUMBER: US/10/282,1122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/194,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-13
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-17
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 70558
 LENGTH: 1051
 TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*
 US-10-282-122A-70558

Query Match 10.2%; Score 104; DB 15; Length 1051;
 Best Local Similarity 25.9%; Pred. No. 15;
 Matches 53; Conservative 29; Mismatches 69; Indels 54; Gaps 11;

Qy 25 QNLISLTENKNOISYKDIENKVSKVLYFNGISDIDLRSKQAKYTVEHFKNGT---- 79
 Db 50 QTMGSGATPQSTQDEBTSKIDQVRSLAYNSVQTE--SIPNASASIVVEVDNGTMDKA 106
 Qy 80 ---XRPVD---LKAGHTADLINTS---DIKAISVNVDTKKQVKDEKARANVQ-VPYT 127
 Db 107 BEQLKKEBDIKFKFDGTVGEPELTNSMDAAPPVAYSETSNRQK-LKDVTKLNQLVPKL 165
 Qy 128 ITVNGTSQNLISLTENKNOISYK-----DLENNPKVSL----- 162
 Db 166 QTIDGV-QN-AQLINGTNPREVSLFKFQRNLDEKGTLANDVENYIKTATRTPGLFQFN 222
 Qy 163 KSNRGITDVLRLSKQAKFTVNFKN 187
 Db 223 KSNKSTV----VDGQFKSVDAFKN 242

RESULT 27
 US-10-369-493-2021
 Sequence 2021, Application US/10369493

PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/252,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application removed - See File Wrapper or PALM.
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 60961
 LENGTH: 1778
 TYPE: PRT
 ORGANISM: Listeria monocytogenes
 us-10-282-122A-60961

Query Match Similarity 10.2%; Score 103.5; DB 15; Length 1778;
 Best Local Similarity 20.2%; Fred. No. 31; Gaps 11;
 Matches 50; Conservative 38; Mismatches 73; Indels 87; Gaps 11;

Qy 17 TITVNGTSQNILLSPNKNQOISYKDIENYKSVLYFNRGISIDD-----
 Db 1014 TVTVNKKDPAPISAKT---EITYDKFSKCTEAAFP---LDDIDADTNDSIVTSNFA 1063
 Qy 63 --LRLSKQAKYTIVFKNGTRVVDLKAGIHPADLINTSDIKASVNVDTKQQ-----
 Db 1064 TAVNLDDKGADTYVTLSINS---DGVAAGTPAAIVHVEKEKIATISTNTAQYERYAKIN 1120
 Qy 113 ---VKDREAKAN-----YQYP--YTTIYNTGTSN-----
 Db 1121 ETQFLKDWHASINASPTTAVLESDFETVVKLDVPGTYVITATNEDEGVYSAPEKSVIV 1180
 Qy 137 -----ILSNLTFFKKNQOISYKDIENYKSVLK-SNRGTT---DVDLRLSKQAKFTV 183
 Db 1181 RKPAPETTADKEITYKFDEVSEAFPLNDIATHISDKNVTAITSNSTDNLNKAGDTV 1240
 Qy 184 NFKNGTKX 191
 Db 1241 TL-NATNE 1247

RESULT 29
 US-09-345-373-30
 Publication No. US20030077695A1
 GENERAL INFORMATION:
 APPLICANT: RUBEN, STEVEN M.
 APPLICANT: JIMENEZ, PABLO
 APPLICANT: DURAN, D. ROXANNE
 APPLICANT: RAMPEY, MARK A.
 APPLICANT: MENDRICK, DONNA
 APPLICANT: ZHANG, JUN
 APPLICANT: NI, JIAN
 APPLICANT: MOORE, PAUL A.
 APPLICANT: COLEMAN, TIMOTHY A.
 APPLICANT: GRUBER, JOACHIM R.
 APPLICANT: DILLON, PATRICK J.
 APPLICANT: GENTZ, REINER L.
 TITLE OF INVENTION: KERATINOCTYE GROWTH FACTOR-2
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 NEW YORK AVE, NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3914
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/345,373
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/023,082
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/461,195
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/023,852
 FILING DATE: 13-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/039,045
 FILING DATE: 28-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/862,432
 FILING DATE: 23-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/910,875
 FILING DATE: 13-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/055,561
 FILING DATE: 13-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFIE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-345-373-30

Query Match Similarity 10.1%; Score 102.5; DB 10; Length 184;
 Best Local Similarity 24.3%; Pred. No. 2.1; Mi matches 61; Indels 41; Gaps 8;
 Matches 41; Conservative 26; Mi matches 61; Indels 41; Gaps 8;

Qy 1 MRGSFHMHMHQSQIPYTITNGTSQNLSSLTENKNQOISYKDIENYKSVLYFN-RGI 58
 Db 1 MRGSFHMHMHGS-----CQALGGDMVSPEATNSSSS-SFSSPSAGRHVRSYNHLQG- 51
 Qy 59 SDIDRLSKQAKYTIFH-----GNR-----GTR-----VVDLKAIGHTADLINTSDIK 101
 Db 52 ---DTRWKLFSFTFYFLKIEKNGKVSTKENCPSILEITSBIGVVAKAINSNYVL 108
 Qy 102 AIS-----VWDTTKQVKDKEAKANQVPTITYNTGTSNQLSN 140
 Db 109 AMNKIGKLYGSKEFNDCUKERIBENGNTYASPNWQHNGRMVALN 157

RESULT 30
 US-10-075-446-30
 Sequence 30, Application US/10075446
 Publication No. US20030129687A1
 GENERAL INFORMATION:
 APPLICANT: RUBEN, STEVEN M.
 APPLICANT: JIMENEZ, PABLO
 APPLICANT: DUAN, D. ROXANNE
 APPLICANT: RAMPEY, MARK A.
 APPLICANT: MENDRICK, DONNA
 APPLICANT: NI, JIAN
 APPLICANT: COLEMAN, TIMOTHY A.
 APPLICANT: GRUBER, JOACHIM R.
 APPLICANT: DILLON, PATRICK J.
 APPLICANT: GENTZ, REINER L.
 TITLE OF INVENTION: KERATINOCTYE GROWTH FACTOR-2
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 NEW YORK AVE, NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3914
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

TITLE OF INVENTION: KERATINOCTYE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS: STEERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/075,446
FILING DATE: 15-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE: Unknown
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: STEFFPE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.03600008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-075-446-30

Query Match Score 10.1%; DB 14; Length 184;
Best Local Similarity 24.3%; Pred. No. 2.1;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Db 1 MRGSHHHHGSGQIPTYITVNGTQNLISSLTFKNQKSYKDIENKVSVLYFN--RGI 58
Db 1 MRGSHHHHHGS-----CQALGQDPRNSPEATNNSSS-SFSSPSAGHRYSYNHLQG- 51

Qy 59 SDIDLRLSKQAKYVIF----KN----GTKR-----VVDLKAGIHTADLINTSDIK 101
Db 52 ---DVRWRKLFSFTKVKSYGKVSGTKKENCPYSILETSVLEGVAVAKAINSNYVL 108

Qy 102 AIS-----VNYDTKQVYKDKEAKANYQVPTITVNGTQNLIQN 140
Db 109 AMNKKGKLYGSKEFNNDCKLKERIEENGNTYNTASYFNWQHNGRQMTVALN 157

RESULT 31
US-10-035-212-30
; Sequence 30, Application US/10035212
; Publication No. US20030186904A1

GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
APPLICANT: Jimenz, Pablo A.
APPLICANT: Duan, D. Roxanne
APPLICANT: Ramps, Mark A.
APPLICANT: Hendrick, Donna
APPLICANT: Zhang, Jun
APPLICANT: Ni, Jian
APPLICANT: Moore, Paul A.
APPLICANT: Colleman, Timothy A.
APPLICANT: Gruber, Joachim R.
APPLICANT: Dillon, Patrick J.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Keratinocyte Growth Factor-2
FILE REFERENCE: 1488.0360000
CURRENT APPLICATION NUMBER: US/10/035,212
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/286,368
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/331,168
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 176
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 184
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PQE60-Cyb337
OTHER INFORMATION: Description of Artificial Sequence: PQE60-Cyb337
US-10-035-212-30

Query Match Score 102.5%; DB 14; Length 184;
Best Local Similarity 24.3%; Pred. No. 2.1;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Qy 1 MRGSHHHHHGSQIPTYITVNGTQNLISSLTFKNQKSYKDIENKVSVLYFN--RGI 58
Db 1 MRGSHHHHHGS-----CQALGQDPRNSPEATNNSSS-SFSSPSAGHRYSYNHLQG- 51

Qy 59 SDIDLRLSKQAKYVIF----KN----GTKR-----VVDLKAGIHTADLINTSDIK 101
Db 52 ---DVRWRKLFSFTKVKSYGKVSGTKKENCPYSILETSVLEGVAVAKAINSNYVL 108

Qy 102 AIS-----VNYDTKQVYKDKEAKANYQVPTITVNGTQNLIQN 140
Db 109 AMNKKGKLYGSKEFNNDCKLKERIEENGNTYNTASYFNWQHNGRQMTVALN 157

RESULT 32
US-10-901-210-30
; Sequence 30, Application US/10901210
; Publication No. US2005003796A1
; GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Keratinocyte Growth Factor-2
FILE REFERENCE: PF155P2D1
CURRENT APPLICATION NUMBER: US/10/901,210
CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION NUMBER: 10/035,212
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,853
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/286,368
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/331,168
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 176
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 184

Query Match Score 101.5; DB 9; Length 3241;
 Best Local Similarity 23.6%; Pred. No. 93; Mismatches 37; Indels 65; Gaps 12;
 Matches 55; Conservative

Qy 10 HGSQIPTYTNGTSQNLISSLTENKQOISYKDIENKVKSLYFNRRGSDIDLRSKOA 69
 Db 165 HGRVENGIPVDGKVK----IPLNPNCSITVEKGKNAVEGI----GLYAADIRL--- 210

Qy 70 KTYVHFNGTKRVDLKGIAHTADLN---TSIDKA-----ISVNVDTRKQVKDKE 117
 Db 211 KDTAILKIG---ITDFKLVLNSDRINGSLTDLKATTKSGDILSAHIDSPQRKANGRN 267

Qy 118 A-----KANVQVPTITYNGT---SNTISNLTFPKK----NOQISYKD 153
 Db 268 STVGKRIEEYVGKNTKANIESDAVLEAGNKNIKSARANTGRPKKEGEKEYNTPLSLSD 327

Qy 154 LENVK----SVLKSNRGT-----DDVDRLSKQAKFTVNFNGTPKVIDL 195
 Db 328 VEASVRVNGKRVIGKVNVDITAEAKNFYDATAL-VTKLAKHSFSFVTGSIISPINL 379

RESULT 36
 Sequence 1, Application US/10647057
 Publication No. US20040047871A1

GENERAL INFORMATION
 APPLICANT: KANSAS STATE UNIVERSITY RESEARCH FOUNDATION
 APPLICANT: NAGARAJA, T.
 APPLICANT: STEWART, GEORGE
 APPLICANT: NARAYANA, SANJEEV
 APPLICANT: CHENGARAPPA, M.

TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN VACCINE AND PRE
 FILE REFERENCE: PCT/30962
 CURRENT APPLICATION NUMBER: US/10/647,057
 CURRENT FILING DATE: 2003-08-22
 NUMBER OF SEQ ID NOS: 15
 SEQ ID NO 1
 LENGTH: 3241
 ORGANISM: Fusobacterium necrophorum

Query Match Score 101.5; DB 15; Length 3241;
 Best Local Similarity 23.6%; Pred. No. 93; Mismatches 37; Indels 65; Gaps 12;
 Matches 55; Conservative

Qy 10 HGSQIPTYTNGTSQNLISSLTENKQOISYKDIENKVKSLYFNRRGSDIDLRSKOA 69
 Db 165 HGRVENGIPVDGKVK----IPLNPNCSITVEKGKNAVEGI----GLYAADIRL--- 210

Qy 70 KTYVHFNGTKRVDLKGIAHTADLN---TSIDKA-----ISVNVDTRKQVKDKE 117
 Db 211 KDTAILKIG---ITDFKLVLNSDRINGSLTDLKATTKSGDILSAHIDSPQRKANGRN 267

Qy 118 A-----KANVQVPTITYNGT---SNTISNLTFPKK----NOQISYKD 153
 Db 268 STVGKRIEEYVGKNTKANIESDAVLEAGNKNIKSARANTGRPKKEGEKEYNTPLSLSD 327

RESULT 37
 Sequence 1, Application US/10193764
 Publication No. US-10-193-764-65

GENERAL INFORMATION
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Yang, Yan-Ping
 APPLICANT: Klein, Michel H.

TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH MOLECULAR WEIGHT PROTEINS
 FILE REFERENCE: 1038-1239MITS
 CURRENT APPLICATION NUMBER: US/10/193,764
 CURRENT FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: 09/167,568
 PRIOR FILING DATE: 1998-10-07
 NUMBER OF SEQ ID NOS: 91
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 65

Query Match Score 101; DB 14; Length 1095;
 Best Local Similarity 23.9%; Pred. No. 26;
 Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

Qy 3 GSHHHHHHGSQLPYTI-----TVNGTSQNLISSLTENKQOISYKDIENKVKS 51
 Db 422 GSDFDNH--QKPLTIKKDVIINSGNLTTAGNNIVAGNLTVESN--ANFKAITNFTFNV 476

Qy 52 --LYFNRGISD-----DLRLSKQAKFTVHFNGTKRVDLKGIAHTADLN-TS 98
 Db 477 GSDFDNRGNSNISIARKGARFDINDSKNLSITNNSSSTYTII-----SGNTINRKNG 529

Qy 99 DIKAISYUNVDTIKKQ----VQDEKAKANQVQPYTTINTGTSQNLISSLTENKQOISYK 152
 Db 530 DLNNTNEGSQDTEMQIGDVSQKEG-----NLTTISDKLNITQDITKAVGDGENSDS 581

Qy 153 DLBNVYKSVLGNSNRGTDVDRLLSKQAKFTVNFNGTPKVIDLKG 198
 Db 582 DATNNANLTITKELKTQDLNISGNKAEITAQDS---DLTIG 623

RESULT 38
 Sequence 2, Application US/10092680
 Publication No. US20020164354A1

GENERAL INFORMATION
 APPLICANT: Barenkamp, Stephen J.
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE HAEMOPHILUS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/092,880
 CURRENT FILING DATE: 2002-03-08
 PRIOR APPLICATION NUMBER: 09/155,614
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 08/617,697
 PRIOR FILING DATE: 1996-04-01
 PRIOR APPLICATION NUMBER: PCT/US97/04707
 PRIOR FILING DATE: 1997-04-01
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 1536

TYPE: PRT
 ORGANISM: Haemophilus influenzae

Query Match Score 101; DB 13; Length 1536;
 Best Local Similarity 23.9%; Pred. No. 40;
 Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

Qy 3 GSHHHHHHGSQLPYTI-----TVNGTSQNLISSLTENKQOISYKDIENKVKS 51
 Db 863 GSDFDNH--QKPLTIKKDVIINSGNLTTAGNNIVAGNLTVESN--ANFKAITNFTFNV 917

52 -LYFNRGISDI-----DLRISQAKYTVHFKNGTKRVVDLKAGIHTADLIN-TS 98
 918 GGLFDNRKNSNIAKGARFKDIDNSKLNTTNSSTYRTII-----SGNTINRNG 970
 99 DIKAISVNDTJKQ---VTDKEAKANVQPYTTINGTSQNLNTPKK--NQQISYK 152
 971 DLNITNEGSDTEMQIGGDSQSKEG-----NLTISSDKINITKQTITRAVGDENSDS 1022
 1023 DATNNANLTIKTKELKLTLTQDLNISGFNKAEITAQDG---DLTIG 1064

RESULT 39
 US-10-193-764-63
 Sequence 63, Application US/10193764
 Publication No. US20030133943A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Yang, Yan Ping
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
 TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
 FILE REFERENCE: 1038-1239M1S
 CURRENT APPLICATION NUMBER: US/10/193_764
 CURRENT FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: 09/167,568
 PRIOR FILING DATE: 1998-10-07
 NUMBER OF SEQ ID NOS: 91
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 63
 LENGTH: 1536
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-193-764-63

Query Match 9.9%; Score 101; DB 14; Length 1536;
 Best Local Similarity 23.9%; Pred. No. 40;
 Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

Qy 3 GSHHHHHHGSQLIPYTI-----TVNGTSQNLTSLTENKNOOISYKDIENKVKS 51
 Db 863 GSDFDNH---QKPLTIKKDVIINSGNLNTAGGNIVNAGNLTVESN--ANPKAITNETENV 917
 Qy 52 -LYFNRGISDI-----DLRISQAKYTVHFKNGTKRVVDLKAGIHTADLIN-TS 98
 Db 918 GGLFDNRKNSNIAKGARFKDIDNSKLNTTNSSTYRTII-----SGNTINRNG 970
 Qy 99 DIKAISVNDTJKQ---VTDKEAKANVQPYTTINGTSQNLNTPKK--NQQISYK 152
 Db 971 DLNITNEGSDTEMQIGGDSQSKEG-----NLTISSDKINITKQTITRAVGDENSDS 1022
 Qy 153 DLNINVRKVLKSNRGTIDVDRISQAKFTVHFKNGTKRVVDLKAG 198
 Db 1023 DATNNANLTIKTKELKLTLTQDLNISGFNKAEITAQDG---DLTIG 1064

Search completed: March 16, 2005, 10:55:25
 Job time : 139 secs

52 -LYFNRGISDI-----DLRISQAKYTVHFKNGTKRVVDLKAGIHTADLIN-TS 98
 918 GGLFDNRKNSNIAKGARFKDIDNSKLNTTNSSTYRTII-----SGNTINRNG 970
 99 DIKAISVNDTJKQ---VTDKEAKANVQPYTTINGTSQNLNTPKK--NQQISYK 152
 971 DLNITNEGSDTEMQIGGDSQSKEG-----NLTISSDKINITKQTITRAVGDENSDS 1022
 1023 DATNNANLTIKTKELKLTLTQDLNISGFNKAEITAQDG---DLTIG 1064

RESULT 40
 US-10-681-171-2
 Sequence 2, Application US/10681171
 Publication No. US20050053618A1
 GENERAL INFORMATION:
 APPLICANT: Barenkamp, Stephen J.
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE
 TITLE OF INVENTION: HAEMOPHILUS
 FILE REFERENCE: 5346
 CURRENT APPLICATION NUMBER: US/10/681,171
 CURRENT FILING DATE: 2003-10-09
 PRIOR APPLICATION NUMBER: 09/155,514
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 08/617,697
 PRIOR FILING DATE: 1996-04-01

Result No.	Score	Query Match Length	DB ID	Description
1	950	93.5	689	Sequence 2, Appli
2	440	43.3	150	Sequence 5, Appli
3	440	43.3	150	Sequence 5, Appli
4	210	20.7	151	Sequence 5, Appli
5	210	20.7	151	Sequence 5, Appli
6	159	15.6	31	Sequence 5, Appli
7	155	15.3	31	Sequence 5, Appli
8	116.5	11.5	512	Sequence 5, Appli
9	114	11.2	211	Sequence 5, Appli
10	110	10.8	31	Sequence 5, Appli
11	110	10.8	1095	Sequence 5, Appli
12	110	10.8	1101	Sequence 5, Appli
13	110	10.8	1220	Sequence 5, Appli
14	110	10.8	1226	Sequence 5, Appli
15	108.5	10.7	288	Sequence 5, Appli
16	106	10.4	345	Sequence 5, Appli
17	104	10.2	74	Sequence 5, Appli
18	104	10.2	159	Sequence 5, Appli
19	104	10.2	1051	Sequence 5, Appli
20	103.5	10.2	609	Sequence 5, Appli
21	102.5	10.1	184	Sequence 5, Appli
22	102.5	10.1	184	Sequence 5, Appli
23	102.5	10.1	184	Sequence 5, Appli
24	101.5	10.0	3241	Sequence 5, Appli
25	101	9.9	1095	Sequence 5, Appli
26	101	9.9	1536	Sequence 5, Appli
27	101	9.9	1536	Sequence 5, Appli

RESULT 2
 US-08-956-171E-5238
 Sequence 5238 Application US/08956171E
 Patent No. 6593114

GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Farnon

TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/781,986A
 FILING DATE: 08/08/1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,1446
 REFERENCE/DOCKET NUMBER: PB248PP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 5238:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-781-986A-5238

Query Match 43 3%; Score 440; DB 4; Length 150;
 Best Local Similarity 78.9%; Pred. No. 2.6e-34;
 Matches 86; Conservatve 13; Mismatches 10; Indels 0; Gaps 0;

Qy 4 SHHHHHGSQLPYTTTGTGSQNLSSLTPEKQDIEENKYSVLYENRGISDIDL 63
 Db 42 SLHHGSQLKVHPYATVNGTSQNLSSLTPEKQDIEENKYSVLYENRGISDIDL 101

RESULT 3
 US-08-781-986A-5238
 Sequence 5238 Application US/08781986A
 Patent No. 6737248

GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/781,986A
 FILING DATE: 08/08/1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,1446
 REFERENCE/DOCKET NUMBER: PB248PP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 5238:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-781-986A-5238

Query Match 43 3%; Score 440; DB 4; Length 150;
 Best Local Similarity 78.9%; Pred. No. 2.6e-34;
 Matches 86; Conservatve 13; Mismatches 10; Indels 0; Gaps 0;

Qy 4 SHHHHHGSQLPYTTTGTGSQNLSSLTPEKQDIEENKYSVLYENRGISDIDL 63
 Db 42 SLHHGSQLKVHPYATVNGTSQNLSSLTPEKQDIEENKYSVLYENRGISDIDL 101

RESULT 4
 US-08-956-171E-5233
 Sequence 5233 Application US/08956171E
 Patent No. 6593114

GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEX/FAX: (301) 308-8439

INFORMATION FOR SEQ ID NO: 5233:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 151 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5233:
 US-08-956-171E-5233

Query Match Score 210; DB 4; Length 151;
 Best Local Similarity 44.3%; Pred. No. 1.9e-12;
 Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

Qy 14 IPYITITNGTSQNILLSSITENKQISYKDIEENKVSKVLYFNRGISDIDLRSKQAKYT 73
 Db 55 VPYTIADGIMAFNQSYLNLPKDSQSYLGNKVALLYDERGVTPEKIRNAKSAYTI 114

Qy 74 HPKNGTRKRVUDLKAGIHTADLNTDIKAISYNVDTK 110
 Db 115 TWKDGSKKEVDLKKDSYTNLFDSNSIKQIDINVTK 151

RESULT 5
 US-08-781-986A-5233
 Sequence 5233, Application US/08781986A
 Patent No. 6717248

GENERAL INFORMATION:
 APPLICANT: Charles Kunisch
 TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08-781-986A-5233

Query Match Score 210; DB 4; Length 151;
 Best Local Similarity 44.3%; Pred. No. 1.9e-12;
 Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

Qy 14 IPYITITNGTSQNILLSSITENKQISYKDIEENKVSKVLYFNRGISDIDLRSKQAKYT 73
 Db 55 VPYTIADGIMAFNQSYLNLPKDSQSYLGNKVALLYDERGVTPEKIRNAKSAYTI 114

Qy 74 HPKNGTRKRVUDLKAGIHTADLNTDIKAISYNVDTK 110
 Db 115 TWKDGSKKEVDLKKDSYTNLFDSNSIKQIDINVTK 151

RESULT 6
 US-08-248-021A-3
 Sequence 3, Application US/08248021A
 Patent No. 5688240

GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Jonsson, Klas
 APPLICANT: Patti, Joseph M.
 APPLICANT: Gurusiddappa, Sivashankarappa

NUMBER OF SEQUENCES: 255

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent-In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,021A
 FILING DATE: 24-MAY-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 3,928
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEX/FAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:

; TOPOLOGY: linear
 US-08-248-021A-3
 Query Match Score 159; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 60 DIDRLRSQAKTVHFKNGTKRVDLKGAIY 90
 Db 1 DIDRLRSQAKTVHFKNGTKRVDLKGAIY 31

RESULT 7
 US-08-248-021A-4
 Sequence 4, Application US/08248021A
 Patent No. 564240
 GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Jonsson, Klas M.
 APPLICANT: Patti, Joseph M.
 APPLICANT: Gurisiddappa, Sivashankarappa
 TITLE OF INVENTION: MHC II ANALOG FROM STAPHYLOCOCCUS AUREUS
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,021A
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: TAWK:155
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-248-021A-4

Query Match Score 155; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e-08;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 170 DVDLRSQAKTVHFKNGTKRVDLKGAIY 200
 Db 1 DVDLRSQAKTVHFKNGTKRVDLKGAIY 31

RESULT 8
 US-08-248-021A-5
 Sequence 5, Application US/08248021A
 Patent No. 564240
 GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Patti, Joseph M.
 APPLICANT: House-Pompeo, Karen
 APPLICANT: Stharam, Narayana
 APPLICANT: Symersky, Jindrich
 APPLICANT: KAPPGSKITV--DNTKTIDV 246

; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
 AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,021A
 FILING DATE: 24-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: TAWK:155
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 512 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-248-021A-6

Query Match Score 116.5; DB 3; Length 512;
 Best Local Similarity 23.8%; Pred. No. 0.0085%; Gaps 14;
 Matches 64; Conservative 29; Mismatches 79; Indels 97; Gaps 14;
 Qy 1 MRGSHHHHHGGSQIETYTTVNGTSSNLLSS-----LTF-NKNOQISYKD-----43
 Db 1 MRGSHHHHHGGSGARDISST-NVTDTIVSFSKIEDGKTYKMTDDKGKIQGDMIRKYA 59

44 -----IENKVSV-----LYN----RGISDDIDRLRSQAKYT 72
 Db 60 WPTSSGTVKIEGYSKTVPLTVRGEQVAVITPDGATITNDKVERLSDV---SGFAEFE 115

73 VHFKNQTKRVDLKGAIHTADLINTSDIKAISV--NVDTKKQVYDKEA-----118
 Qy 116 VQGRNLTO-----TNTSDDKVATITSGNKETNTVTHKSEAGTSSVYKNG 161

Db 119 -----KANVQVPTTITVNGTSQNLLNFTKK---NQQLSYKDLENVV---KSVTLKSNR 166

162 DMLPDTTHWFLNNEKSVSKDITKQIQGGQOLDLSTLNINVGTGHSNYSGQS 221

167 GITDPLRSQAKETVNFNGTKRVDLKGAIY 195

Db 222 AITDFE-KAPPGSKITV--DNTKTIDV 246

RESULT 9
 US-08-248-021A-7
 Sequence 4, Application US/08248021A
 Patent No. 564240
 GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Patti, Joseph M.
 APPLICANT: House-Pompeo, Karen
 APPLICANT: Stharam, Narayana
 APPLICANT: Symersky, Jindrich
 APPLICANT: KAPPGSKITV--DNTKTIDV 246

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: U.S.

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,253

FILING DATE: Concurrently Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,678

FILING DATE: 16-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33 928

REFERENCE/DOCKET NUMBER: TAMK:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 418-1577

INFORMATION FOR SEQ ID NO: 4 :

SEQUENCE CHARACTERISTICS:

LENGTH: 211 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-856-253-4

Query Match 11.2%; Score 114; DB 3; Length 211;

Best Local Similarity 23.9%; Pred. No. 0_0042; Indels 60; Gaps 10;

Matches 54; Conservative 28; Mismatches 84; Indels 60; Gaps 10;

Qy 1 MRGSHHHHHGSGQIPTTYTNGTSQNLISSLTKENQOISYKDIENTKVSVLYNFRGKSD 60

Db 1 MRGSHHHHHGSGDDKVATITSG-----NKSTNVTVKSEAGTSSVFPYKIG--- 46

Qy 61 IDLRLSKQAKYTWHFKNGTKRVDLKGAIHTADLINTS--DIKAISWNV----- 107

Db 47 -DNL-PBDTHYRWFELNNKEYSVSKDITKIDQIQQQLDLSTLNINVGTGHSNYSG 104

Qy 108 -----DTKKQYKDKKEAKANTQVPTI-TVNGTSQNLSNIT-----FKNQQ 148

Db 105 QSAITDFEKAFFPSKITTNTNTIDVTPQGYGSNSFSINYKTKTNEQQKEFVNNSQ 164

Qy 149 ISYKD---LENNYKSV-----LKSNRGSDTVD--DIRLSKOAKFT 182

Db 165 AWYQEHGKEEVNGKSFNHTVHNINANAGIEGTVKGEKLXKVLQDKDT 210

RESULT 10 US-08-248-011A-7

Sequence 7, Application US/08248021A

Patent No. 564220

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Johnson, Klas

APPLICANT: Patti, Joseph M.

APPLICANT: Gurusiddappa, Sivashankarappa

TITLE OF INVENTION: MRC II ANALOG FROM STAPHYLOCOCCUS AUREUS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/248,021A

FILING DATE: 24-MAY-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33, 928

REFERENCE/DOCKET NUMBER: TAMK:155

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 7 :

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-248-021A-7

Query Match 10.8%; Score 110; DB 4; Length 1095;

Best Local Similarity 25.1%; Pred. No. 0_1;

Matches 50; Conservative 29; Mismatches 76; Indels 44; Gaps 8;

Qy 18 ITYNGISONLISLT-----FNKQQISYKDIENTKVSVLYNFRGJSDIDLRSKQAKY 71

Db 446 LTVGSAINTERNLNTVEGSKAPLANYNSF-----VSGLFNDQKSNIST----AKG 494

Qy 72 TVHK--NGTRVVDLKAGIHTADLINTSD-----IAKSVNVTKQVKDKEAKAVQ 123

Db 495 GAHFIDINNTK-----SLNTTNSDSAYRTTLEGNTNSGDLNTDNKNNAEIQ 544

Qy 124 VPYTI-----TVNGTSQNLNTFFK--NQQSYKDLENNVSVLKSNRGITDYLDR 174

Db 545 IGGNISOKEGNLTSSDSDKINNTQITKGVNEDDSSTANNANLTIKTBLQLTGDLN 604

Query Match Score 110; DB 4; Length 1220;
 Best Local Similarity 23 %; Pred. No. 0.12;
 Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

Qy 175 LSKOAKFTVNEKNGTKKVI 193
 Db 605 ISGFDKAITEAKAGDLII 623

RESULT 12
 US-09-206-942-43
 ; Sequence 43, Application US/09206942
 ; Patent No. 6432669
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
 ; TITLE OF INVENTION: Molecular Weight Proteins
 ; FILE REFERENCE: 1038-861 MIS-Jb
 ; CURRENT APPLICATION NUMBER: US/09/206,942
 ; CURRENT FILING DATE: 1998-12-08
 ; CURRENT FILING DATE: 1998-10-07
 ; EARLIER APPLICATION NUMBER: 09/167,568
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 43
 ; LENGTH: 1101
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 ; US-09-206-942-43

Query Match Score 110; DB 4; Length 1101;
 Best Local Similarity 25.1%; Pred. No. 0.11; Mismatches 76; Indels 44; Gaps 8;

Qy 18 ITVNGTSONILSSIT----ENKNOQSYKDIENKVSKVLYFNRGTSIDILRLSKQAY 71
 Db 452 LTVTGSANIEKNLTLVEGSAFKLNPNSFN-----VSGLFDNQGKNSI-----AKG 500

Qy 72 TVHFK--NGTKRVDLKGAGHTADLINTSD----IAISVNVDIKQVKDKEAKANVQ 123
 Db 501 GAHKFDINTNK-----SUNITNTSDSAYRTIIEGNITNSGNDLNKNAEIQ 550

Qy 124 VPTI-----TVNGTSONILSNLTFKK--NQIISTKDLENVKSVLKSNRGITDYL 174
 Db 551 IGGNISQEGNLTISSDKINITQITKGVNKEDSDSTANNANLTIKTKELOLTDLN 610

Qy 175 LSKOAKFTVNEKNGTKKVI 193
 Db 611 ISGFDKAITEAKAGDLII 629

RESULT 13
 US-09-206-942-28
 ; Sequence 28, Application US/09206942
 ; Patent No. 6432669
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
 ; TITLE OF INVENTION: Molecular Weight Proteins
 ; FILE REFERENCE: 1038-861 MIS-Jb
 ; CURRENT APPLICATION NUMBER: US/09/206,942
 ; CURRENT FILING DATE: 1998-12-08
 ; EARLIER FILING DATE: 1998-10-07
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 28
 ; LENGTH: 1220
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 ; US-09-206-942-28

Query Match Score 110; DB 4; Length 1226;
 Best Local Similarity 23 %; Pred. No. 0.12; Mismatches 82; Indels 64; Gaps 9;

Qy 3 GHSHHHHHGSQLQPYTI----TVNGTSONILSSITFNKQQISYKDIENKVSKV 51
 Db 428 GSDFDNH--QKPLTIKDVTLNSNLTAGNVININGNTVANGANL--KAITHTFNV 482

Qy 52 -LYFNRGSDIDLRSKQAKYTVFHKNGTKRVDLKGAGHTADLINTSDKINITQITKGV 109
 Db 483 GGLFDNKGNNSI-----ARGGAKFDINTNSLN-ITTNSDT 520

Qy 110 KQQ-----VTDKEAKANVQVPTI-----TVNGTSONILSNLTFKK-- 145
 Db 521 TYRTILEGNITNKAGDLNIIDNKGAEIQIGGNISQEGNLTISSDKINITQITKGV 580

Qy 146 NQIISTKDLENVKSVLKSNRGITDYLRSKQAKFTVNPNRGTKVI 193
 Db 581 NKEDDSSTANNANLTIKTKELOLTDLNISGFDKAEITAKEGDLII 628

RESULT 14
 US-09-206-942-26
 ; Sequence 26, Application US/09206942
 ; Patent No. 6432669
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
 ; TITLE OF INVENTION: Molecular Weight Proteins
 ; FILE REFERENCE: 1038-861 MIS-Jb
 ; CURRENT APPLICATION NUMBER: US/09/206,942
 ; CURRENT FILING DATE: 1998-12-08
 ; EARLIER APPLICATION NUMBER: 09/167,568
 ; EARLIER FILING DATE: 1998-10-07
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 26
 ; LENGTH: 1226
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 ; US-09-206-942-26

Query Match Score 110; DB 4; Length 1226;
 Best Local Similarity 23 %; Pred. No. 0.12; Mismatches 82; Indels 64; Gaps 9;

Qy 3 GHSHHHHHGSQLQPYTI----TVNGTSONILSSITFNKQQISYKDIENKVSKV 51
 Db 428 GSDFDNH--QKPLTIKDVTLNSNLTAGNVININGNTVANGANL--KAITHTFNV 482

Qy 52 -LYFNRGSDIDLRSKQAKYTVFHKNGTKRVDLKGAGHTADLINTSDKINITQITKGV 109
 Db 483 GGLFDNKGNNSI-----ARGGAKFDINTNSLN-ITTNSDT 520

Qy 110 KQQ-----VTDKEAKANVQVPTI-----TVNGTSONILSNLTFKK-- 145
 Db 521 TYRTILEGNITNKAGDLNIIDNKGAEIQIGGNISQEGNLTISSDKINITQITKGV 580

Qy 146 NQIISTKDLENVKSVLKSNRGITDYLRSKQAKFTVNPNRGTKVI 193
 Db 581 NKEDDSSTANNANLTIKTKELOLTDLNISGFDKAEITAKEGDLII 628

RESULT 15
 US-09-134-001C-4005
 ; Sequence 4005, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIORITY NUMBER: 1998-08-13
; PRIORITY FILING DATE: 1998-08-13
; PRIORITY NUMBER: US 60/064,964
; PRIORITY FILING DATE: 1997-11-08
; PRIORITY NUMBER: 1997-11-08
; PRIORITY FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4005
; LENGTH: 288
; TYPE: PRT
; ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-4005

Query Match 10.7%; Score 108.5;, DB 3; Length 288;
Best Local Similarity 20.6%; Pred. No. 0.022%;
Matches 43; Conservative 43; Mismatches 78; Indels 49; Gaps 6;

Qy 9 HFGSQIPTYITVNGTSONILLSLTENKNOQISYKDIENKVSVLYFNRGSDIDLRSKQ 68
Db 28 NNGKVTIGVSNDTK----AWEVKELAKKD-----DIDLEIKHF 64

Qy 69 AKYTIVHFKNGTRVVDLKAGTA-----DLINTSDIKAIASVNVDTKQVK 114
Db 65 SDYNPVNPALKSGLDIDINAFQHAFDQLQYKAHKDNTNEALSTVPLGIYSDKVNPK 124

Qy 115 DKEAKANVQVQIPTYITVNGTQSQNLSN--LTFFKNNQI - SYKDLENNSV-----L 162
Db 125 DVKGQAQVAIPDVDSNQARAKLLESAGLKLKCNFLGNGTKDIESNPDKLKIKAQDQ 184

Qy 163 FSNRGITDWDRLSKQAKFTNFNGTKVVDLK 196
Db 185 QTARALSDVDISVNNNGVATKAGDAKKDPYLE 218

RESULT 16
US-08-856-253-7
Sequence 7, Application US/08856253
; Patent No. 6288214
GENERAL INFORMATION:
; APPLICANT: Hook, Magnus M.
; APPLICANT: Parti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Smersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 8
; NUMBER OF METHODS OF USE: 8
; CORRESPONDENCE ADDRESS:
; STREET: Arnold, White & Durkee
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY /AGENT INFORMATION:
; NAME: Mitchell, Barbara S.
; REGISTRATION NUMBER: 33,9228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-7

Query Match 10.4%; Score 106; DB 3; Length 345;
Best Local Similarity 23.3%; Pred. No. 0.048%;
Matches 52; Conservative 35; Mismatches 90; Indels 46; Gaps 11;

Qy 1 MRGSHHHHHGSQLIPTYITVNGTS-QNLSSLTENKNOQIS-YKDIENKVSVLYP---N 55
Db 1 MRGSHHHHHGSMVAADAPAAAGTDITNQLTNVTVGIDSQTIVPHQAGYKLNQYFSVPN 60

Qy 56 RGSDIDDLRSKQAKYTVFKNGTKVVDLKAG-----IHT-ADLNT-S 98
Db 61 SAVKGDTFKITVPKELNLNGVTSPAKVPPIMAGDQVLANGVIDSDGGNVYTPDVTNTKD 120

Qy 99 DIKAI-----SVNDTQKQVQDKEAKANVQV-----YTTIVNTSQNI 137
Db 121 DVKATLTMAYIOPENVRKIGNVTLATGJGSTANKTVLDYERKGFTNLSKGTIDQI 180

Qy 138 -LSNLTFKKNQOISYKDLENNNSVLSKSN-RGITDVDLRSKQ 178
Db 181 DKTNNTYROTIVNPGS-DNVIAPLTGNLKPNTDSNALIDQ 222

RESULT 17
US-09-490-291-11
Sequence 11, Application US/09490291
; Patent No. 6620917
GENERAL INFORMATION:
; APPLICANT: Melio, Charlene M.
; APPLICANT: Arcidiacono, Steven
; TITLE OF INVENTION: No. 6620917tel Purification and Fiber Spinning Technique
; TITLE OF INVENTION: Protein Fibers
; FILE REFERENCE: ARMY-06665
; CURRENT APPLICATION NUMBER: US/09/490,291
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 74
; TYPE: PRT
; ORGANISM: *Nephila clavipes*
US-09-490-291-11

Query Match 10.2%; Score 104; DB 4; Length 74;
Best Local Similarity 30.7%; Pred. No. 0.0884%;
Matches 31; Conservative 27; Indels 34; Gaps 3;

Qy 1 MRGSHHHHHGSQLIPTYITVNGTSQNLSSLTENKNOQISYKDIENKVSVLYP 60
Db 1 MRGSHHHHHGGS-----MASGDLKRNKVAQLKRYRSLKD 34

Qy 61 IDLRSKQAKYTVFKNGTKVVDLKAGHTADLINTSDIK 101
Db 35 -----KAELKQEVSRLENEIEDLAKAKI-GDINNTSGIR 67

RESULT 18
US-08-856-253-2
Sequence 2, Application US/08856253
; Patent No. 6288214
GENERAL INFORMATION:
; APPLICANT: Hook, Magnus M.
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Smersky, Jindrich
; TELEPHONE: (512) 418-3000

8

Db 457 -----SFKNBRKKVLDLR 469

RESULT 21
US-09-023-082A-10
Sequence 30, Application US/09023082A
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANE
APPLICANT: RAMPE, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZL, REINER L.

TITLE OF INVENTION: KERATINOCTYE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023, 082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 50/023, 852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 50/039, 045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8/862, 432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8/910, 875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 50/055, 561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36, 688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-082A-30

Query Match Score 102.5; DB 3; Length 184;
Best Local Similarity 24.3%; Pred. No. 0.043;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Qy 1 MRGSRRHHHHSQIPTYTNGTSNLLSITFNKQQISYKDIEBNKVSVLYFN--RG1 58
Db 1 MRGSRRHHHHS-----COALGQDMVSPEATNSSS-SFSSPSSAGHRVRSYHQLQG- 51

Qy 59 SDIDRLSKQAKYTHF---KN----GTR-----VVDLRAGIHTADLNTSDIK 101
Db 52 ---DWRWLKFSLFTKFLKEBNGKVSGTKKENCPYSILETSVIGWVAKAINSNYL 108

Qy 102 AIS-----VVYDTKQVKDKEAKANQVPTTYTNGTSQNLSN 140
Db 109 AMNKCKLGSKEFFNDCKLKERIENGNTYASFNWOHNGROMYVALN 157

RESULT 22
US-09-248-998-10
Sequence 30, Application US/09248998
GENERAL INFORMATION:
PATENT NO. 659879
APPLICANT: Jimenez, Pablo
APPLICANT: Rampy, Mark A.
APPLICANT: Mendrick, Donna
APPLICANT: Russell, Deborah
APPLICANT: Louise, Arthur
TITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2
FILE REFERENCE: 1498.160002
CURRENT APPLICATION NUMBER: US/09/248,998
CURRENT FILING DATE: 1999-02-12
EARLIER APPLICATION NUMBER: US 60/114,387
EARLIER FILING DATE: 30-DEC-1998
EARLIER APPLICATION NUMBER: US 60/074,585
EARLIER FILING DATE: 13-FEB-1998
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-248-998-10

Query Match Score 102.5; DB 4; Length 184;
Best Local Similarity 24.3%; Pred. No. 0.043;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Qy 1 MRGSRRHHHHSQIPTYTNGTSNLLSITFNKQQISYKDIEBNKVSVLYFN--RG1 58
Db 1 MRGSRRHHHHS-----COALGQDMVSPEATNSSS-SFSSPSSAGHRVRSYHQLQG- 51

Qy 59 SDIDRLSKQAKYTHF---KN----GTR-----VVDLRAGIHTADLNTSDIK 101
Db 52 ---DWRWLKFSLFTKFLKEBNGKVSGTKKENCPYSILETSVIGWVAKAINSNYL 108

Qy 102 AIS-----VVYDTKQVKDKEAKANQVPTTYTNGTSQNLSN 140
Db 109 AMNKCKLGSKEFFNDCKLKERIENGNTYASFNWOHNGROMYVALN 157

RESULT 23
US-09-610-651-30
Sequence 30, Application US/09610651
GENERAL INFORMATION:
PATENT NO. 6693077
APPLICANT: Ruben, Steven M.
APPLICANT: Jimenez, Pablo
APPLICANT: Duan, D. Roxanne
APPLICANT: Rampy, Mark A.
APPLICANT: Mendrick, Donna
APPLICANT: Zhang, Jun
APPLICANT: Ni, Jian

RESULT 24
US-09-841-786-1
; Sequence 1, Application US/09841786
; GENERAL INFORMATION:
; APPLICANT: NAGARAJA, T. G.
; APPLICANT: STEWART, GEORGE C.
; APPLICANT: NARAYANAN, SANJEEV K.
; APPLICANT: CHENGAPPA, M. M.
; TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
; TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
; FILE REFERENCE: 30296
; CURRENT APPLICATION NUMBER: US/09/841,786
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/558,257
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 3241
; TYPE: PRT
; ORGANISM: Fusobacterium necrophorum
US-09-841-786-1

Query Match 10.0%; Score 101.5; DB 4; Length 3241;
Best Local Similarity 23.6%; Pred. No. 3.1;
Matches 55; Conservative 37; Mismatches 76; Indels 65; Gap 54;

Qy 10 HGSQIPTYITNGTSQNILSSLTFNKNQQLSYKDIENKVSKVLYFNRGSDIDRLRSKQ
Db 165 HGKVENGIPYDGVK---IPLAPNGSITVEGKINAVEGI---GLYAADRL--
Qy 70 KYTVHKNGTKTRVVDLKGAIHTADLNN---TSDIKA-----ISVNYDTKQVKD
Db 211 KDTAIATKRG---ITDFKLNLYSDRINSLGTLKATPKSGDILLSAHDSPQKAMG
Qy 118 A-----KANVQPYITIVNGT--SONILSNLTFKK----NQOISY
Db 268 STVGKRIEEVYKGNTKANTIESDAVLEADGNIKISAKATNGRFKKEGEKTYNTPLSL
Qy 154 LENNVK---SVLKSNRGIT-----DVDLRLSQAKFTVNFKNGTKVIDL 195
Db 328 VEASVRYNKGVIGKVNQKDITAEAKNFYDFTL-VTKLAKRSFSVTGTSISPINL 379

RESULT 25
US-09-206-942-69
; Sequence 69, Application US/09206942
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; Molecular Weight Proteins
; FILE REFERENCE: 1038-061 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; EARLIER APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 69
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-69

Query Match 10.1%; Score 102.5; DB 4; Length 184;
Best Local Similarity 24.3%; Pred. No. 0.043;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Qy 1 MRGSHHHHGSQLPYITIVNGTSQNILSSLTFNKNQQLSYKDIENKVSKVLYFN--RGI 58
Db 1 MRGSHHHHGSQLPYITIVNGTSQNILSSLTFNKNQQLSYKDIENKVSKVLYFN--RGI 58
Qy 59 SDIDRLRSKOAKYVHF---RN---GTKR-----VVDLKGAIHTADLNTSDIK 101
Db 52 --DVRWRKLFSFKYFLKIEKGKVS GTKRNCPCSYLLEITSVIEGVAVAINSYVL 108

Query Match 9.9%; Score 101; DB 4; Length 1095;
Best Local Similarity 23.9%; Pred. No. 0.75;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gap 54;

Qy 102 AIS-----YNDTOKVKDKEAVANVQPYITIVNGTSQNILSN 140
Db 109 AMNKGKGLYGSKEPNNDCKLEREAGNTYASFNWHGRMONYVNL 157

3 GSHHHHHGSQLPYTI-----TNGTSQNLSSLTENKNQOISYKDIENKYKVSV 51
 Db 422 GSFEDNH---QKLTIKKDVIINSGNLTAGGNIVNAGNLTVESN--ANFKAITNFTFNV 476

Qy 52 -LYFNRSISDI-----DLRLSKOAKTYVHFKNGTKRVDLKGIAHTADLIN-TS 98
 Db 477 GGFDFNKNSNISIAKGARFKDIDNSNLSSITNNSSSTYRTI-----SGNITKNG 529

Qy 99 DIKAISVNVDTKQ---VKDKEAKANVQVPYTITNGTSQNLSSLTPEKK--NQQISYK 152
 Db 530 DLNTNEGSDDTEQIGGDSQREG-----NLTTISDKINTKQITIKAGVDGENSDS 581

Qy 153 DLENVVKCPLKSNRGITYDLRLSKOAKFTVKNGTKKVIDLKAG 198
 Db 582 DATNNANTIKTKEKLTLQDLNSGFKNAEITAQDG-----DITIG 623

RESULT 27
 Sequence 2, Application US/08302632
 Patent No. 5603938
 GENERAL INFORMATION:
 APPLICANT: Barenkamp, Stephen J
 ATTORNEY: ST. GEME LII, JOSEPH W
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
 NUMBER OF SEQUENCES: 8
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/302,832
 FILING DATE: 16-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9205704.1
 FILING DATE: 16-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US pct/us93/02166
 FILING DATE: 16-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Berkstresser, Jerry W
 REGISTRATION NUMBER: 22,651
 REFERENCE DOCKET NUMBER: 1038-404
 TELECOMMUNICATION INFORMATION:
 NAME: BERKSTRESSER, JERRY W
 REGISTRATION NUMBER: 22, 651
 REFERENCE DOCKET NUMBER: 1038-293
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 415-0810
 TELEFAX: (703) 415-0813
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1536 amino acids
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: DNA (genomic)
 US-08-302-632-2

Query Match 9.9%; Score 101; DB 1; Length 1536;
 Best Local Similarity 23.9%; Pred. No. 1,2; Matches 54; Indels 54; Gaps 11;

Qy 3 GSHHHHHGSQLPYTI-----TNGTSQNLSSLTENKNQOISYKDIENKYKVSV 51
 Db 863 GSFEDNH---QKLTIKKDVIINSGNLTAGGNIVNAGNLTVESN--ANFKAITNFTFNV 917

Qy 52 -LYFNRSISDI-----DLRLSKOAKTYVHFKNGTKRVDLKGIAHTADLIN-TS 98
 Db 918 GGFDFNKNSNISIAKGARFKDIDNSNLSSITNNSSSTYRTI-----SGNITKNG 970

Qy 99 DIKAISVNVDTKQ---VKDKEAKANVQVPYTITNGTSQNLSSLTPEKK--NQQISYK 152
 Db 971 DLNTNEGSDDTEQIGGDSQREG-----NLTTISDKINTKQITIKAGVDGENSDS 1022

Qy 153 DLENVVKCPLKSNRGITYDLRLSKOAKFTVKNGTKKVIDLKAG 198

RESULT 28
 US-08-530-198-2
 Sequence 2, Application US/08530198
 ; GENERAL INFORMATION:
 ; APPLICANT: BARENKAMP, STEPHEN J
 ; PATENT NO. 5869065
 ; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
 ; TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Shoemaker and Mattare, Ltd.
 ; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202-0286
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/469,880
 ; FILING DATE: 06-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9205704.1
 ; FILING DATE: 16-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/302,832
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berkstresser, Jerry W
 ; REGISTRATION NUMBER: 22,651
 ; REFERENCE/DOCKET NUMBER: 1038-516 MIS:vg
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 415-0810
 ; TELEFAX: (703) 415-0813
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1536 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-469-880-2

Query Match 9.9%; Score 101; DB 2; Length 1536;
 Best Local Similarity 23.9%; Pred. No. 1.2;
 Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

Qy 3 GHSHHHHHGSGQIPTYI-----TUNGTSONILLSLTENKNOQISYKDIENKVSKV 51
 Db 863 GSDFDNH---QKPLTIKDVINSGNLTAGGNVTNIAGNLTVESN-ANFKAITNFENV 917

Qy 52 -LYFNRGISDI-----DIRLSKQAKYTIVHKNGTKRVDLKGIAHTADLN-TS 98
 Db 918 GGLFDIKGNNSNISIAGCGARFKDIDNSRNLSITNTSSSTYRTI-----SGNTINKNG 970

Qy 99 DIAKISVNDTJKQ---VRDKEAKANTQVPTITVNQTSNQLSNUTFKK--NQQISYK 152
 Db 971 DLNITNEGSDDTENQIGGDVSQREG----NLTISSDKINITKQITIKAGVDGENSDS 1022

Qy 153 DLENVKSYLKSRGITYDLRSKQAKFTVNFKNGTKVIDLKAG 198
 Db 1023 DATNNANLTIKTKEKLTDLNISGFNKAEITAQDS---BLTIG 1064

RESULT 30
 US-08-72B-470-2
 ; Sequence 2, Application US/08728470
 ; Patent No. 5928651
 ; GENERAL INFORMATION:
 ; APPLICANT: Barenkamp, Stephen J

TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: Of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
CITY: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0386
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berklesser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE DOCKET NUMBER: 1018-633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
TYPE: amino acid
STRANDEDNESS: single

-08-728-470-2
 SULT 31
 Sequence 2, Application US/08617697
 Patent No. 5973356
 GENERAL INFORMATION:
 APPLICANT: Barenkamp, Stephen J
 TITLE OF INVENTION: High Molecular Weight Surface Proteins
 Query Match 9.9%; Score 101; DB 2; Length 1536;
 Best Local Similarity 23.9%; Pred. No. 1.2;
 Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;
 Matches 54; Mismatches 32; Indels 86; Gaps 11;
 3 GSHHHHHGSQLPYYTI-----TVNQTSQNQLLSSLTFNQKQIQSYKDIENKVKS 51
 863 GSDFDNH---QKPLTIIKKDVILNSGNITAGNIVNAGNLTVESN--ANPQAITNFTENV 917
 52 - LYFRRG1SDI-----DLRJSQAKQYTVHFPNGTKRVDLIGAHTADLNN-TS 98
 918 GGLFDKGNSNSISIAKGGARPKDIDSKNLSSITNTNSSTRTII----SGNTINNG 970
 99 DIKAISVNVDTTKQ----VRDKEAKANQVQPYTIVTGTNTGSNQNLSTFKK--NQGQSYK 152
 971 DLNITNGSDTEMQIGGDVSQREG-----NLT1SSDKINITQDITIAGVGDNNSDS 1022
 153 DLENNYTKVLSKNSNRGTTDVLRLSKQAKFTNPKNGTKKVKYIDLKAG 198
 1023 DATNNANLTIKTKEKLTLTODLNIGGPNKAETAKDGS---DLTIG 1064

TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Shoemaker and Mattare, Ltd.
 STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202-0286
 COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/08/617,697
 i FILING DATE: 01-APR-1996
 i CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 i APPLICATION NUMBER: US 08/302,832
 i FILING DATE: 05-OCT-1994
 PRIORITY APPLICATION DATA:
 i APPLICATION NUMBER: US PCT/US93/02166
 i FILING DATE: 16-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 i NAME: Berkestrasser, Jerry W
 i REGISTRATION NUMBER: 22,651
 i REFERENCE/DOCKET NUMBER: 1038-557
 TELECOMMUNICATION INFORMATION:
 i TELEPHONE: (703) 415-0810
 i TELEFAX: (703) 415-0813
 i INFORMATION FOR SEQ ID NO: 2:
 i SEQUENCE CHARACTERISTICS:
 i LENGTH: 1536 amino acids
 i TYPE: amino acid
 i STRANGLINES: single
 i TOPOLOGY: linear
 i MOLECULE TYPE: DNA (genomic)
 US-08-617-697-2

Query Match 9.9%; Score 101; DB 2; Length 15
 Best Local Similarity 23.9%; Pred. No. 1, 2;
 Matches 54; Conservative 32; Mismatches 86; Indels 18

Qy	3 GSHHHHHHGSQIPTYI-----TWNQTSQNLSSLTPNKNQQQ	
Db	863 GSDPDNH--QKPLTIKDVLINSGNLTAGGNTVNIAGNTVESN--A	
Qy	52 -LYFNRCISDI-----DLRLSQAQKTYVHFNGTKVVDLKA	
Db	918 GGFLPDNKNSNISTAKGGARFKDIDNSKLSSITNNSSSTYRTII-----	
Qy	99 DIKAISVNDTJKQ---VRDKEAKANQVPTTIVNGTSQNLNSLNLL	
Db	971 DLNTNEGSTENIQGGDSQREG-----NLTISSDKINTKQTII	
Qy	153 DLENNPKVSLKNSNRGITYDRLLSKOAKFTPKNGTKVVDLKG 1	
Db	1023 DATNNANITKTRKELKTDQDLNISGFNRAETARDGS----DLTIG 1	

RESULT 32
 US-08-719-641-2
 Sequence 2, Application US/08719641
 GENERAL INFORMATION:
 i APPLICANT: Barenkamp, Stephen J
 i TITLE OF INVENTION: High Molecular Weight Surface Proteins
 i TITLE OF INVENTION: Of No. 6218141-Typeable Haemophilus
 i NUMBER OF SEQUENCES: 10
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: Shoemaker and Mattare, Ltd.

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0296
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,641
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Beretreever, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: S-08/719-641-2

```

; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09-1167, 568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 67
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-67

Query Match          9.9%; Score 1
Best Local Similarity 23.9%; Prod. N
Matches 54; Conservative 32; Misn
      3 GSHHHHHHGGSQIPYTI-
Db      863 GSPFDNH--QKPLTIKKDVIINSGLN
Qy      52 -LYENRGISDI-----DLRLS
Db      918 GGLFDNKGNSNTISIAKGARPKDIDNS
Qy      99 DIKAISVNVNDTQQKQ---VVKDEAKAN
Db      971 DLNITNEGSDTMEOIQGDVSSREG---V
Qy      153 DLLENNTKVSLKNSNRGTTDVDLRSLSKOA
Db      1023 DATNNVNLTKTKEKLKTQDLNISGFNFN

RESULT 34
US-09-976-594-4
; Sequence 4, Application US/09976594
; Patient No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240, 409
; PRIOR FILING DATE: 2000-11-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
SEQ ID NO 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 667744
US-09-976-594-4

Query Match          9.8%; Score 1
Best Local Similarity 24.0%; Prod. N
Matches 48; Conservative 36; Misn
      21 NGTSQNLISSLTNKQNOQSYKDIENT
Db      331 NGNLDFTLISFLKSN-TLPISLQSIRS
Qy      76 KNGTCKRYDLKAGIHTADLINTEDIK
Db      388 RGTEAV----GYFLNLIDSMSDSD
Qy      136 NIL-----SNLTFF
Db      441 NLKESYHYPELIIKDAHLIVESKQLDR
Qy      178 QAKFTVNPKNGTKKVIDLKA 197

```

Db 497 QLIVLCESEENMQKALEJKA 516 RESULT 35
 US-10-030-031A-2
 / Sequence 2, Application US/10030031A
 / Patent No. 6746847
 / GENERAL INFORMATION
 / APPLICANT: Vermeer, Cas
 / TITLE OF INVENTION: Diagnostic Assay for Human Matrix
 / Glu-Protein and Its Use as A Biomarker
 / FILE REFERENCE: 13176PCUTS
 / CURRENT APPLICATION NUMBER: US/10/030,031A
 / CURRENT FILING DATE: 2002-07-16
 / PRIOR APPLICATION NUMBER: PCT/EP00/06173
 / PRIOR FILING DATE: 2000-07-02
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: FabSeq for Windows Version 4.0
 / SEQ ID NO: 2
 / LENGTH: 297
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE: Protein encoded by Sequence 1 containing 6-His tag
 / OTHER INFORMATION: - DHFR - linker (=4 amino acids) - MGP
 us-10-030-031A-2

Query Match Score 9.6%; DB 4; Length 297;
 Best Local Similarity 40.7%; Pred. No. 0.25;
 Matches 24; Conservative 7; Mismatches 17; Indels 11; Gaps 4;

Qy 1 MRGSHHHHHHGGI---PYITIVNGTSQNILSSLTFKRNQQISYKDLENKVKSVLNR 56
 Db 1 MRGSHHHHHHGGIMVRPLN-SIVAVSQN---MGIGKNDLPWPPLRNEFK--YFQR 51

RESULT 36
 US-09-248-796A-15901
 / Sequence 15901, Application US/09248796A
 / Patent No. 6747137
 / GENERAL INFORMATION
 / APPLICANT: Keith Weinstock et al
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 / FILE REFERENCE: 107196-132
 / CURRENT APPLICATION NUMBER: US/09/248,796A
 / CURRENT FILING DATE: 1999-02-12
 / PRIOR APPLICATION NUMBER: US/98-02-13
 / PRIOR FILING DATE: 1998-08-13
 / NUMBER OF SEQ ID NOS: 28208
 / LENGTH: 333
 / TYPE: PRT
 / ORGANISM: Candida albicans
 us-09-248-796A-15901

Query Match Score 9.6%; DB 4; Length 333;
 Best Local Similarity 20.5%; Pred. No. 0.3;
 Matches 38; Conservative 47; Mismatches 59; Indels 41; Gaps 7;

Qy 12 S0IPYTIVNG-----TSONILSSLTFKRNQQISYKDLENKVKSVLYNRGISDIDL 63
 Db 84 SVVPKTLKVNP1KITSNLTDKKIHACKSYNSLS-SWKELINQ----- 126
 Qy 64 RLSKQAKTVTHFKNG-TKRVVD----LKAGIHTADLINTSDIKAISSVNVDTKKQVKDKE 117
 Db 127 -----SYDIEYKRETRQQIBEHRAKICELIMITLDDNNMLSDDDDEDNDKYBEEEQ 180
 Qy 118 AKANVQVPTYTIVNGTSQNILSNLTFKRNQQISYKD--LENNVRSVLSNLTKRNQQISYKD-- 174

Db 181 LNANGEKDYSLSSINKPNKIKTKT-KRNKELKHKERVKLEQEIKDUKQLQKDLNLDEI 239
 Qy 175 LSKQA 179
 Db 240 LEKQA 244

RESULT 37
 US-09-604-588-1
 / Sequence 1, Application US/09604958
 / Patent No. 6615460
 / GENERAL INFORMATION
 / APPLICANT: HIJUM, SACHA ADRIANUS FOKKE TACO
 / APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
 / APPLICANT: DIJGHUIZEN, LUBERT
 / APPLICANT: RAHAOUI, HAKIM
 / TITLE OF INVENTION: NOVEL FRUCTOSYLTRANSFERASES
 / FILE REFERENCE: BO 43667-ACW
 / CURRENT APPLICATION NUMBER: US/09/604,958
 / CURRENT FILING DATE: 2000-06-28
 / NUMBER OF SEQ ID NOS: 50
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 1
 / LENGTH: 789
 / TYPE: PRT
 / ORGANISM: Lactobacillus reuteri
 us-09-604-588-1

Query Match Score 9.5%; DB 4; Length 789;
 Best Local Similarity 24.9%; Pred. No. 1.3;
 Matches 48; Conservative 31; Mismatches 87; Indels 27; Gaps 8;

Qy 19 TUNGTSONILSSLTFKRNQQISYKDLENKVKSVLYNRGISDIDLRLS--SKOAKYT 72
 Db 24 TVNAGADTNEN-NDSSTVQTTGNDIAKSVTGLSGQVSAASDTTIRTSANANSASSA 82
 Qy 73 VHFKNKGTKRVD--LKAGIHTADLINTSDIKAISSVNVDT-KKQVKDKEAKAN----VQV 124
 Db 83 ANTONENSQVASSAAITSTSRAASINNTDQKAQENTNTAKNDTQKAAPANESEAKN 142
 Qy 125 PYTTINGTS-----QNLISNLTKRNQQISYKDLENKVKSVLNRGITDVDLRSLK 177
 Db 143 EPAVVNDSSAAKNDQQSKKNTAKLN----DQAENVVKKAGIDPNSLTDDQIKALN 197
 Qy 178 QAKFTVNFKNGT 190
 Db 198 KMNPSSKAAKSGTQ 210

RESULT 38
 US-09-995-587A-1
 / Sequence 1, Application US/09995587A
 / Patent No. 6730502
 / GENERAL INFORMATION
 / APPLICANT: VAN HIJUM, SACHA ADRIANUS FOKKE TACO
 / APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
 / APPLICANT: DIJGHUIZEN, LUBERT
 / TITLE OF INVENTION: NOVEL FRUCTOSYLTRANSFERASES
 / CURRENT APPLICATION NUMBER: US/09/995,587A
 / CURRENT FILING DATE: 2002-02-28
 / PRIOR APPLICATION NUMBER: 09/604,958
 / FILE REFERENCE: BO43667-CIP
 / PRIOR FILING DATE: 2000-06-28
 / PRIOR APPLICATION NUMBER: EPO 00201872.9
 / PRIOR FILING DATE: 2000-05-25
 / NUMBER OF SEQ ID NOS: 40
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 1
 / LENGTH: 789
 / TYPE: PRT
 / ORGANISM: Lactobacillus reuteri

Query Match 9.5%; Score 96.5; DB 4; Length 789;
 Best Local Similarity 24.9%; Pred. No. 1.3;
 Matches 48; Conservative 31; Mismatches 87; Indels 27; Gaps 8;

Qy 19 TVNGTSONLSSLTFNKNQQSYKDIENKTKVSLYFNRGI---KQAXT 72
 Db 24 TVNASDTLNEN-NDSSTVQTTGNDIATKSVTLGSGGSAASDPTTTSANANSASA 82
 Qy 73 VHFKNQTKRVD---LKAQHTADLINTSDIKAIWSVDT-KKQVKDKEAKAN -- YGV 124
 Db 83 ANTONSNQVASSAAATTSSTSSAASUNNTDSKAQAENTTAKDOKAPANESSEAKN 142
 Qy 125 PYTITNGTS-----ONILSNTLPFKQNOQSYKDLENNNSVLSK 177
 Db 143 EPAVNNDSSAAKNDQSSKKNTTAKLN---KDAENVVKAGIDPNSLTDDQIKALN 197

Qy 178 QAKPTYNFKNTH 190
 Db 198 KNFNSKAAKSGTQ 210

RESULT 39
 / Sequence 19, Application US/08621081A
 / Patent No. 5795974

/ GENERAL INFORMATION:
 / APPLICANT: Cole, Barry C.
 / APPLICANT: Atkin, Curtis L.
 / APPLICANT: Knudson, Kevin L.
 / APPLICANT: Sawitzke, Allan D.
 / TITLE OF INVENTION: Mycoplasma Arthritis Superantigen
 / NUMBER OF SEQUENCES: 32
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Thorpe, No. 5795974th & Western
 / STREET: 9035 South 700 East, Suite 200
 / CITY: Sandy
 / STATE: Utah
 / COUNTRY: USA
 / ZIP: 84070

/ COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 / COMPUTER: IBM ThinkPad 340
 / OPERATING SYSTEM: MS-DOS 6.22
 / SOFTWARE: Word Perfect 6.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/621,081A
 / FILING DATE:
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/165,038
 / FILING DATE: December 10, 1993
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Alan J. Howarth
 / REGISTRATION NUMBER: 36,553
 / REFERENCE/DOCKET NUMBER: T676.CIP/U-1195
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (801)566-6633
 / INFORMATION FOR SEQ ID NO: 19:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 221 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein

US-08-621-081A-19

Query Match 9.4%; Score 95.5; DB 1; Length 221;
 Best Local Similarity 20.9%; Pred. No. 0.26;
 Matches 45; Conservative 35; Mismatches 64; Indels 71; Gaps 9;

Qy 3 GSHHHHHHGSQLPYTIVNGTSQNLSSLTENKNQQISYKDIENKVKSYLYPNRGISDID 62

Db 2 GHHHHHHMKLRY-----ENPKRAQKHVVNNVVFTNKEELEDI- 40
 Qy 63 LRLSKQAKTYHFRKGTRKV-----DLKAGHTADLINTSDIKAI 103
 Db 41 -----YNLSNKETKEVFLKFKLKVNFYRHAFFGLVNDYNGLLEYKEIFNMMPFL-L 91
 Qy 104 SVNVDTQKQVKDKEAKANQVPTIVNGTSQNLSSLTENKNQQISYKDIENKVKSYLVK 163
 Db 92 SVFDTQK---KGEANNEQIERNIA-----ILDEIMAKADNDLSYFISON----K 134
 Qy 164 SNRGITDYLRSKQAKPTVNPFNGTKVVDIKAG 198
 Db 135 NFOELWDKAVLTKTEMKIKL---KGQK--LDLRDG 164

RESULT 40
 / Sequence 33,08, Application US/09107433
 / Patent No. 6800744

/ GENERAL INFORMATION:
 / APPLICANT: Lynn A. Doucette-Stamm and David Bush
 / TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID
 / SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 / FOR DIAGNO

/ NUMBER OF SEQUENCES: 5206
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 / STREET: 100 Beaver Street
 / CITY: Waltham
 / STATE: Massachusetts
 / COUNTRY: USA
 / ZIP: 02454

/ COMPUTER READABLE FORM:
 / MEDIUM TYPE: CD-ROM ISO9660
 / COMPUTER: <Unknown>
 / OPERATING SYSTEM: <Unknown>
 / SOFTWARE: <Unknown>
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/107,433
 / FILING DATE: 30-Jun-1998
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: 60/ 085131
 / FILING DATE: May 12, 1998
 / APPLICATION NUMBER: 60/01553
 / FILING DATE: July 2, 1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Arinello, Pamela Deneke
 / REGISTRATION NUMBER: 40,89
 / REFERENCE/DOCKET NUMBER: GTC-011
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (781)853-5007
 / TELEFAX: (781)853-8227
 / INFORMATION FOR SEQ ID NO: 3308:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 331 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: YES
 / ORIGINAL SOURCE:
 / ORGANISM: Streptococcus pneumoniae
 / FEATURE:
 / NAME/KEY: misc. feature
 / LOCATION: (B) LOCATION 1...331
 / SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

US-09-107-433-3308

Query Match 9.4%; Score 95; DB 4; Length 331;
 Best Local Similarity 22.9%; Pred. No. 0.51;
 Matches 54; Conservative 32; Mismatches 64; Indels 86; Gaps 13;

Qy 3 GSHHHHHHGSQLPYTIVNGTSQNLSSLTENKNQQISYKDIENKVKSYLYPNRGISDID 62

```

Db      68 GDHYHYNG-KVBYDALP---SEBLMK---DPNYQLKDAIVNEVKGGY-----IIVD 115
Qy      63 LRLSKOAKXTVHEKNGTRVVDLKAGITHADLINTSDIKAI5VNVDTKQVKDKE---- 117
Db      116 -----GKVYVTLKDAAH-----ADNVRTKD----EINROKOJEHVKDNEKYNSN 154
Qy      118 -AKANVOVPYT-----ITVNGTSQNL-----SNLT 142
Db      155 VAYARSQRYYTMDGYVNPAIDIETNAYITVPHGGHYYPKSDU.SASEIAAKAHLA 214
Qy      143 PFKNQ-QISYKDL-ENVKSYLKSNGITDVDRLSKOAQFTVNPKNGTKVID 194
Db      215 GRNMQPSQSYSSSTASDNTQSVAKGS-----TSKPANKSENQSLKELYD 261

```

Search completed: March 16, 2005, 10:44:10
 Job time : 45 secs

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Run on:	March 16, 2005, 10:36:37 ; Search time 168 Seconds (without alignments)	
Scoring table:	BLOSUM62	460.429 Million cell updates/sec
Title:	US-10-041-775-2	
Perfect score:	1016	Gapop 10.0 , Gapext 0.5
Sequence:	1 MRGSHHHHGGSOIPIYTIV.....FTVNFKNGTKKVIDLKAGIY 200	
Total number of hits satisfying chosen parameters:	2105692	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0\$ Maximum Match 100\$	
	Listing first 4 summaries	
Database :	A_Geneseq_16Dec04:*	RESULT 1
	1: GeneseqP1980:*	ABP58754
	2: GeneseqP1990:*	ID ABP58754 standard; protein; 200 AA.
	3: GeneseqP2000:*	XX
	4: GeneseqP2001:*	AC ABP58754;
	5: GeneseqP2002:*	XX
	6: GeneseqP2003:*	DT 03-APR-2003 (first entry)
	7: GeneseqP2003b:*	XX
	8: GeneseqP2004:*	XX
		DB Recombinant Staphylococcus aureus Map19.
		XX Map19; Map; major histocompatibility complex class II analogue protein; recombinant; T-cell mediated response; prevention; modulation; T-cell overstimulation; toxic shock syndrome; poison ivy; T-cell lymphoproliferative disease; leukaemia; autoimmune disease; delayed-type hypersensitivity response DTH; staphylococcal infection; immunomodulator; immuno suppressive; cytostatic; vaccine.
		XX KW
		OS Synthetic.
		OS
		XX
		PN WO200277010-A2.
		XX
		PD 03-OCT-2002.
		XX
		PP 10-JAN-2002; 2002WO-US000401.
		XX
		PR 10-JAN-2001; 2001US-0265023P.
		XX
		PA (TEXA) UNIV TEXAS A & M SYSTEM.
		XX
		PI Brown EN, Lee LY, Hook M;
		XX
		XX WPI; 2003-046760/04.
		DR N-PSPB; ABZ25399.
		XX
		PT New method of preventing or modulating T-cell-mediated response in a host, useful for e.g. the treatment of toxic shock syndrome, comprises administering a Staphylococcus aureus major histocompatibility complex class II analog protein.
		PT
		CC The invention relates to a novel method of preventing or modulating a T-cell mediated response in an individual involving the administration of the Staphylococcus aureus major histocompatibility complex class II antigenic fragments such as Map19 (ABP58754) or its active fragments Map19 and Map10 (ABP58755). Map, and its active fragments Map19 and Map10, may be used to treat or prevent pathogenic conditions associated with
Result No.	Score	Query
-	-	-
1	1016	ABP58754
2	950	AAW26301
3	886.5	AA027181
4	818.5	AAE71428
5	626	AAE25524
6	626	ABP58755
7	440	AAW89790
8	210	ABM73216
9	210	ABW89795
10	159	AAW26302
11	155	AAW26303
12	142	ABJ19003
13	142	ABP73460
14	135	ABM71429
15	133	ABM79016
16	131	ABM79017
17	117.5	ABB79627
18	117.5	ABP71275
19	117.5	ADM86524
20	116.5	ABM79015
21	115	ABW31554
22	114.5	ABU44119
23	114.5	ABB79625
24	114.5	ABP71273
25	114.5	ADM86520

overstimulation of T cells such as toxic shock syndrome or poison ivy, and C cell lymphoproliferative diseases such as leukaemia and autoimmune disease. They may also be used to reduce delayed-type hypersensitivity (DTH) responses and to prevent or modulate a T-cell mediated response to a staphylococcal infection. The present sequence represents recombinant Map19.

Sequence 200 AA:
 Query Match 100.0%; Score 1016; DB 6; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.8e-80;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSHHHHHHSQIPTITVNGTSQNLLSSTFNKQQISYKDIEVKSVLYFNRGISD 60
 Db 1 IDLRLSKQAKTIVHFNGTKRVDLKGAGIHTADLINTSDIKAISSVNVTQKVDKEAKA 120
 Qy 61 IDLRLSKQAKTIVHFNGTKRVDLKGAGIHTADLINTSDIKAISSVNVTQKVDKEAKA 60
 Db 61 IDLRLSKQAKTIVHFNGTKRVDLKGAGIHTADLINTSDIKAISSVNVTQKVDKEAKA 120
 Qy 121 NVQVPITITVNGTSQNLLSNTFKKNOQISYKDLENNVKSVLKSNSRGITVYDLRSKQK 180
 Db 121 NVQVPITITVNGTSQNLLSNTFKKNOQISYKDLENNVKSVLKSNSRGITVYDLRSKQK 180
 Qy 181 FTVNFKNGTKRVDLKGAGIY 200
 Db 181 FTVNFKNGTKRVDLKGAGIY 200

RESULT 2
 AAW26301 standard; protein; 689 AA.
 AC AAW26301;
 XX DT 17-OCT-2003 (revised)
 DT 16-NOV-1997 (First entry)

DE Staphylococcal MHC class II antigen analogue protein.
 XX MHC II analogue protein; major histocompatibility complex;
 KW staphylococcal; adhesin; virulence factor; vaccine.
 XX OS Staphylococcus aureus; strain FDA 574.

FH Key Location/Qualifiers
 Peptide 1..30
 FT /label= sig_peptide
 Protein 31..689
 FT /label= Mat_protein

XX PN US5648240-A.
 XX DR 1997-372059/34.
 XX DR N-PSDB; AAT84441.
 XX PR 24-MAY-1994; 94US-00248021.
 XX PA (TEXA) UNIV TEXAS A & M.
 XX PI Jonsson K, Hook M, Patti JM, Gurusiddappa S;
 XX DR 1997-372059/34.
 XX DR N-PSDB; AAT84441.
 XX PT DNA encoding Staphylococcus aureus broad spectrum adhesin - for
 PT production of recombinant adhesin for use in vaccines.
 XX PS Claim 17; Col 11-14; 30pp; English.
 XX CC This protein sequence comprises a broad spectrum adhesin of

CC Staphylococcus aureus FDA 574 that is capable of binding fibronectin or
 CC vitronectin and which includes six repeated segments containing MHC II
 CC mimicking units (see AAW26302-07) of about 30 amino acid residues.
 CC Studies of the binding specificities of the adhesin show that it
 CC functionally resembles an MHC II antigen in that it binds synthetic
 CC peptides. Vectors incorporating DNA (see AAT84441) encoding the adhesin
 CC can be used to express recombinant adhesin in transformed host (esp.
 CC bacterial, partic. E. coli) cells. Recombinant adhesin can be used in
 CC vaccines against staphylococcal infections. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 689 AA;
 Query Match 93.5%; Score 950; DB 2;
 Best Local Similarity 97.0%; Pred. No. 8.3e-74;
 Matches 191; Conservative 1; Mis matches 5; Indels 0; Gaps 0;
 XX SQ Sequence 689 AA;

Query Match 93.5%; Score 950; DB 2;
 Best Local Similarity 97.0%; Pred. No. 8.3e-74;
 Matches 191; Conservative 1; Mis matches 5; Indels 0; Gaps 0;

Qy 4 SHHHHHHHSQIPTITVNGTSQNLLSSTFNKQQISYKDIEVKSVLYFNRGISDIDL 63
 Db 41 SLHRRGYSKIQIPTITVNGTSQNLLSSTFNKQQISYKDIEVKSVLYFNRGISDIDL 100

Qy 64 RLSKQAKTIVHFNGTKRVDLKGAGIHTADLINTSDIKAISSVNVTQKVDKEAKA 123
 Db 101 RLSKQAKTIVHFNGTKRVDLKGAGIHTADLINTSDIKAISSVNVTQKVDKEAKA 160

Qy 124 VPYTITVNGTSQNLLSNTFKKNOQISYKDLENNVKSVLKSNSRGITVYDLRSKQKFTV 183
 Db 161 VPYTITVNGTSQNLLSNTFKKNOQISYKDLENNVKSVLKSNSRGITVYDLRSKQKFTV 220

Qy 184 NFKNQGTKRVDLKGAGIY 200
 Db 221 NFKNQGTKRVDLKGAGIY 237

RESULT 3
 AAO27181
 ID AAO27181 standard; protein; 657 AA.
 XX AC AAO27181;
 AC AAO27181;
 XX DT 17-SEP-2003 (first entry)
 XX DE Staphylococcus aureus p70 protein, member of the EAP family.
 XX KW EAP; extracellular adherence protein; anti-inflammatory; fibrinogen;
 KW ICAM-1; radiation allergen; sunburn; asthma; psoriasis; encephalitis;
 KW meningitis; osteomyelitis; gingivitis; pancreatitis; antiadhesive;
 KW cancer therapy; atherosclerosis; rheumatoid arthritis; strain wood 46.
 XX OS Staphylococcus aureus.
 XX FH Key Location/Qualifiers
 FT Region 22..50
 FT /note= "Repeat region 1"
 FT Region 131..159
 FT /note= "Repeat region 1"
 FT Region 332..362
 FT /note= "Repeat region 2"
 FT Region 437..477
 FT /note= "Repeat region 2 with a partial 10 residue overlap
 of repeat region 1"
 FT Region 542..572
 FT /note= "Repeat region 2"
 XX PN WO2003041726-A1.
 XX PD 22-MAY-2003.
 XX PR 14-NOV-2002; 2002WO-SE002075.

XX PR 16-NOV-2001; 2001SE-00003831.
 XX PR 16-NOV-2001; 2001US-0331455P.
 XX PR 21-NOV-2001; 2001US-0331782P.

XX (BIOS-) BIOSTAPRO AB.
 XX PA
 XX PI Flock J, Herrmann M, Preissner KT, Chavakis T,
 XX DR WPI: 2003-468585/44.
 PT Use of extracellular adherence protein for the manufacture of anti-inflammatory or antitumor drug in the treatment of e.g. atherosclerosis.
 PT Disclosure; Page 6; 22pp; English.
 XX This invention relates to the use of extracellular adherence proteins (EAPs) are used for antiinflammatory purposes to treat acute or chronic inflammation. Proteins of the EAP family are produced by the bacterium Staphylococcus aureus (S. aureus) and are able to bind to S. aureus cells and agglutinate them. This invention, however, relates to the ability of EAP to bind adhesive proteins in the connective tissue and on cell surfaces, such that it blocks the inflammatory response of the infected host organism. Specifically EAP can bind fibrinogen in the extracellular matrix or ICAM-1 on cells to inhibit the mobility, infiltration and activities of granulocytes, macrophages and lymphocytes. Note that the inflammatory disorders can be from either a bacterial or non-bacterial source and could include responses to radiation, infection, chemicals, allergens and injury. As such EAP can be used as an antiinflammatory to treat various conditions including sunburn, asthma, allergy, psoriasis, encephalitis, meningitis, osteomyelitis, gingivitis and panreatitis. Furthermore, the antiadhesive potential of EAP provides a method for cancer therapy and treatment of atherosclerosis and rheumatoid arthritis caused by uncontrolled cellular extravasation of leukocytes. This polypeptide sequence is the Staphylococcus aureus strain Wood 46 p70 protein, which is a typical member of the EAP family of the invention
 XX Sequence 657 AA;
 SQ Query Match 87.3%; Score 886.5; DB 6; Length 657;
 Best Local Similarity 90.8%; Pred. No. 2.6e-68;
 Matches 177; Conservative 8; Mismatches 9; Indels 1; Gaps 1;
 Qy 6 HHHHRSQQIPITVNTGSQNLSSLTFKNNQISYKDIEVKVSKVLYFNGRISDIDRL 65
 Db 13 HHGHSNTQIPIPTITVNTGSQNLSSLTFKNNQISYKDIEVKVSKVLYFNGRISDIDRL 72
 Qy 66 SKQAKYTIVHFNGTTRVVDLKGAGTAHDINTSDIKAIASVNDTKQVQDKKEAKANVQP 125
 Db 73 SKQABFTVHFNGTTRVVDLKGAGTAHDINTSDIKAIASVNDTKQVQDKKEAKANVQP 131
 Qy 126 YTTVNTGSQNLSSLTFKNNQISYKDLENNVKSVLKSNRGITDVDLRSLSKQAKFTVNP 185
 Db 132 YTTVNTGSQNLSSLTFKNNQISYKDLEDRVKSYLENSRGITDVDLRSLSKQAKFTVNP 191
 Qy 186 KNGTKRKVTDLKGAGIY 200
 Db 192 KNGTKRKVTDLKGAGIY 206
 RESULT 4
 ID ABM71428 standard; protein; 584 AA.
 XX AC ABM71428;
 XX DT 20-NOV-2003 (first entry)
 XX DB Staphylococcus aureus protein #668.
 XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.
 XX OS Staphylococcus aureus.
 XX PN WO200294868-A2.
 XX PN WO200234788-A1.
 XX ID AAE25524 standard; protein; 131 AA.
 XX AC AAE25524;
 XX DT 04-NOV-2002 (first entry)
 XX DB Staphylococcus aureus Map10 protein.
 XX KW Map10 protein; infection; immunological response; passive immunisation;
 KW vaccine; antibacterial.
 XX OS Staphylococcus aureus.
 PN WO200234788-A1.
 XX ID AAE25524 standard; protein; 131 AA.
 XX AC AAE25524;
 XX DT 04-NOV-2002 (first entry)
 XX DB Staphylococcus aureus Map10 protein.
 XX KW Map10 protein; infection; immunological response; passive immunisation;
 KW vaccine; antibacterial.
 XX OS Staphylococcus aureus.
 PN WO200234788-A1.
 XX ID AAE25524 standard; protein; 131 AA.
 XX AC AAE25524;
 XX DT 04-NOV-2002 (first entry)
 XX DB Staphylococcus aureus Map10 protein.
 XX KW Map10 protein; infection; immunological response; passive immunisation;
 KW vaccine; antibacterial.
 XX OS Staphylococcus aureus.
 PN WO200234788-A1.
 XX ID AAE25524 standard; protein; 131 AA.
 XX AC AAE25524;

XX XX XX PP 27-MAR-2002; 2002WO-IB002637.
 PN PD 30-JUL-1997. XX PR 27-MAR-2001; 2001GB-00007661.
 XX XX XX PA (CHIR-) CHIRON SPA.
 PP 07-JAN-1997; 97EP-00100117.
 XX PR 05-JAN-1996; 96US-0009861P.
 PA PI Massignani V, Mora M, Scarbelli M;
 XX XX XX WPI; 2003-120786/11.
 PA DR N-PSDB; ACF74776.
 XX PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or preventing *Staphylococcus* infection, specifically an infection caused by *S. aureus*, e.g. sepsis.
 XX PT
 XX PS Claim 1; SEQ ID NO 4912; 49pp; English.
 PT PS
 XX The invention relates to novel genes and encoded proteins from *S. aureus* protein, a *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to *Staphylococcus* bacteria, specifically an infection caused by *S. aureus*. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel *S. aureus* proteins of the invention.
 XX Sequence 144 AA;
 CC Query Match Score 210; DB 6; Length 144;
 CC Best Local Similarity 44.3%; Pred. No. 2.3e-10;
 CC Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
 CC
 CC Qy 14 IPYTIVNGTQNIISSLTPNKQISYKDENTKSVLYFNRGSDIDRLSKQKTYV 73
 CC Db 48 VPYTIAVDGIMAFNQSYLNLPKDSQISYLDIGNKTYALDERTVPEKLRNAKSAYTI 107
 CC Sequence 144 AA;
 CC Query Match Score 210; DB 6; Length 144;
 CC Best Local Similarity 44.3%; Pred. No. 2.3e-10;
 CC Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
 CC
 CC Qy 14 IPYTIVNGTQNIISSLTPNKQISYKDENTKSVLYFNRGSDIDRLSKQKTYV 73
 CC Db 48 VPYTIAVDGIMAFNQSYLNLPKDSQISYLDIGNKTYALDERTVPEKLRNAKSAYTI 107
 CC Sequence 150 AA;
 CC Query Match Score 440; DB 2; Length 150;
 CC Best Local Similarity 78.9%; Pred. No. 2.4e-30;
 CC Matches 86; Conservative 13; Mismatches -10; Indels 0; Gaps 0;
 CC
 CC Qy 4 SHHHHHHGSGQIPTYTIVNGTSQNLSSLTENKQOQTSYKDENTKSVLYFNRGSDIDL 63
 CC 42 SLHGGTSKVHPAITYVNGTSQNLSSLTENKQOQTSYKDLEDYRVSLSDRGSDIDL 101
 CC
 CC Qy 64 RLSKQDKYTVTHFKNGTKRVIDLKAGHTADINTSDIKASVNTDKQ 112
 CC Db 102 RLSKQDKYTVTHFKNGTKRVIDLKAGHTADINTSDIKASVNTDKQ 150
 CC Sequence 150 AA;
 CC Query Match Score 440; DB 2; Length 150;
 CC Best Local Similarity 78.9%; Pred. No. 2.4e-30;
 CC Matches 86; Conservative 13; Mismatches -10; Indels 0; Gaps 0;
 CC
 CC Qy 4 SHHHHHHGSGQIPTYTIVNGTSQNLSSLTENKQOQTSYKDENTKSVLYFNRGSDIDL 63
 CC 42 SLHGGTSKVHPAITYVNGTSQNLSSLTENKQOQTSYKDLEDYRVSLSDRGSDIDL 101
 CC
 CC Qy 64 RLSKQDKYTVTHFKNGTKRVIDLKAGHTADINTSDIKASVNTDKQ 112
 CC Db 102 RLSKQDKYTVTHFKNGTKRVIDLKAGHTADINTSDIKASVNTDKQ 150
 RESULT 8
 ABMM73216 ID ABM73216 standard; protein; 144 AA.
 AC ABM73216;
 XX DT 20-NOV-2003 (first entry)
 XX DB Staphylococcus aureus protein #2456.
 XX
 KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.
 OS Staphylococcus aureus.
 XX
 KW HUMAN GENOME SCI INC.
 PN Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 PN WO200294868-A2.
 XX
 PD 28-NOV-2002.

PT	production of recombinant adhesin for use in vaccines.	
XX	XX	
PT	Claim 17; Col 13-16; 30pp; English.	
PT	XX	
PS	Claimed peptides (AAW26302-07) correspond to subsegments of repeat units of a broad-spectrum adhesin (see AAW26301) of <i>Staphylococcus aureus</i> FDA.	
XX	CC	
CC	These subsegments show high homology with eukaryotic MHC Class II antigens. They can be used in claimed compositions to induce an immune response to <i>S. aureus</i> in an animal. (Updated on 17-OCT-2003 to standardise OS field)	
CC	XX	
CC	Sequence 31 AA;	
CC	Query Match 15.6%; Score 159; DB 2; Length 31;	
CC	Best Local Similarity 100.0%; Pred. No. 7.9e-07;	
CC	Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC	Qy 60 DIDRLISKQAKYTVPFKNGTKRVDLKAGIH 90	
CC	Db 1 DIDRLISKQAKYTVPFKNGTKRVDLKAGIH 31	
XX	RESULT 11	
XX	AAW26303 standard; peptide; 31 AA.	
XX	AAW26303 ID	
XX	AAW26303 XX	
XX	AC AC	
XX	DT 17-OCT-2003 (revised)	
XX	DT 16-NOV-1997 (first entry)	
XX	DE Staphylococcal MHC class II antigen analogue repeat subsegment 2.	
XX	DE	
XX	MHC II analogue protein; major histocompatibility complex;	
XX	staphylococca; adhesin; virulence factor; vaccine.	
XX	XX	
XX	Staphylococcus aureus; strain FDA 574.	
XX	OS OS	
XX	PN PN	
XX	XX	
XX	PD 15-JUL-1997.	
XX	XX	
XX	PF 24-MAY-1994; 94US-00248021.	
XX	XX	
PR 24-MAY-1994; 94US-00248021.	XX	
XX	XX	
PA (TEXA) UNIV TEXAS A & M.	XX	
XX	XX	
PI Jonsson K, Hook M, Patti JM, Gurusiddappa S;	XX	
XX	XX	
DR WPI; 1997-372059/34.	XX	
XX	XX	
PT DNA encoding Staphylococcus aureus broad spectrum adhesin - for production of recombinant adhesin for use in vaccines.	XX	
PS Claim 17; Col 15-16; 30pp; English.	XX	
XX	XX	
CC Claimed peptides (AAW26302-07) correspond to subsegments of repeat units of a broad-spectrum adhesin (see AAW26301) of <i>Staphylococcus aureus</i> FDA.	XX	
CC	These subsegments show high homology with eukaryotic MHC Class II antigens. They can be used in claimed compositions to induce an immune response to <i>S. aureus</i> in an animal. (Updated on 17-Oct-2003 to standardise OS field)	XX
CC	XX	
CC	Sequence 31 AA;	XX
CC	Query Match 15.3%; Score 155; DB 2; Length 31;	XX
CC	Best Local Similarity 100.0%; Pred. No. 1.8e-06;	XX
CC	Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
CC	Qy 170 DVDLRSKQAKFTVNFKNGTKRVDLKAGIY 200	XX
CC	Db 1 DVDLRSKQAKFTVNFKNGTKRVDLKAGIY 31	XX
XX	RESULT 10	
XX	AAW26302 standard; peptide; 31 AA.	
XX	AAW26302 ID	
XX	AAW26302 XX	
XX	DT 17-OCT-2003 (revised)	
XX	DT 16-NOV-1997 (first entry)	
XX	DB Staphylococcal MHC class II antigen analogue repeat subsegment 1.	
XX	DB	
XX	MHC II analogue protein; major histocompatibility complex;	
XX	staphylococca; adhesin; virulence factor; vaccine.	
XX	XX	
XX	Staphylococcus aureus; strain FDA 574.	
XX	US5648240-A.	
XX	(TEXA) UNIV TEXAS A & M.	
XX	XX	
XX	PN PN	
XX	XX	
XX	15-JUL-1997.	
XX	XX	
XX	24-MAY-1994; 94US-00248021.	
XX	XX	
XX	24-MAY-1994; 94US-00248021.	
XX	XX	
XX	US5648240-A.	
XX	(TEXA) UNIV TEXAS A & M.	
XX	XX	
XX	Jonsson K, Hook M, Patti JM, Gurusiddappa S;	
XX	XX	
DR WPI; 1997-372059/34.	XX	
XX	XX	
PT DNA encoding Staphylococcus aureus broad spectrum adhesin - for	XX	

RESULT 12

ABJ19003 Standard; protein; 141 AA.
 XX ABJ19003;
 XX DT 06-MAR-2003 (First entry)
 XX DE Pathogen specific antigen related staphylococcal protein SEQ ID No 221.
 XX KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 XX KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 XX KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 XX KW autoimmune disease; HIV; hepatitis.
 OS Staphylococcus sp.
 PN WO200259148-A2.
 XX PD 01-AUG-2002.
 XX PP 21-JAN-2002; 2002WO-EP000546.
 XX PR 26-JAN-2001; 2001AT-00000130.
 XX PA (CIST-) CISTEN BIOTECHNOLOGIES GMBH.
 PI Meinke, A., Nagy, E., Von Ahsen, U., Klade, C., Henicus, T., Zauner, W.;
 PI Minh DB, vtyvyska O., Etz H., Dryla A., Weichhart T., Hafner M.;
 PI Tempeimair B;
 XX DR WPI; 2003-075410/07.
 XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 PS Example 7; Page 186; 252PP; English.
 XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against S. aureus or S. epidermidis. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against S. aureus or S. epidermidis. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HRV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 XX Sequence 141 AA;

RESULT 13

ABM73460 Standard; protein; 141 AA.
 XX ABM73460;
 XX DT 20-NOV-2003 (First entry)
 XX DE Staphylococcus aureus protein #2700.
 XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 XX KW enzymatic assay; antibiotic target.
 OS Staphylococcus aureus.
 PN WO200294868-A2.
 XX PD 28-NOV-2002.
 XX PP 27-MAR-2002; 2002WO-IB002637.
 XX PR 27-MAR-2001; 2001GB-00007661.
 XX PA (CHIR-) CHIRON SPA.
 PI Mastagnani, V., Mora, M., Scarselli, M.;
 XX DR WPI; 2003-120786/11.
 DR N-PSDB; ACP75020.

Query Match

14 IPYTITVNGTSONISSLTENKVNQISYKDIEVKSVLYFNRGISDIDRLSKQAKTV 73
 14 VPYTISVDGITALHRTYFIPFBNKVYQEDSKVNELASQRGVYTEKINNAQPATYTL 106
 74 HFKNGTKRYVDLKGHTADLINTSDIKAIHSVNV 107

Best Local Similarity

14.0%; Score 142; DB 6; Length 141;
 Best Local Similarity 33.0%; Pred. No. 0_00018;
 Matches 31; Conservative 25; Mismatches 38; Indels 0; Gaps 0;

RESULT 14

ABM71429 Standard; protein; 96 AA.
 XX AC ABM71429;
 XX DT 20-NOV-2003 (First entry)

Query Match

14 IPYTITVNGTSONISSLTENKVNQISYKDIEVKSVLYFNRGISDIDRLSKQAKTV 73
 47 VPYTISVDGITALHRTYFIPFBNKVYQEDSKVNELASQRGVYTEKINNAQPATYTL 106
 74 HFKNGTKRYVDLKGHTADLINTSDIKAIHSVNV 107

Best Local Similarity

14.0%; Score 142; DB 6; Length 141;
 Best Local Similarity 33.0%; Pred. No. 0_00018;
 Matches 31; Conservative 25; Mismatches 38; Indels 0; Gaps 0;

XX	Staphylococcus aureus protein #669.	PF 05-MAR-2003; 2003WO-US006415.
DE	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;	XX 05-MAR-2003; 2003US-036324P.
KW	enzymatic assay; antibiotic target.	XX (INHI-) INHIBITEX INC.
KW	Staphylococcus aureus.	PA (TEXA) UNIV TEXAS A & M SYSTEM.
OS		XX
XX	W0200294868-A2.	PI Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;
PN		PI Robbins J, Vernachio J, Bowden MG;
XX	28-NOV-2002.	XX WPI; 2003-722324/68.
XX	PP 27-MAR-2002; 2002WO-IB002637.	DR N-PSDB; ACP80325.
PR	27-MAR-2001; 2001GB-00007651.	XX New antibody recognizing a Staphylococcus epidermidis protein comprising SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for treating or preventing a coagulase-negative staphylococcal infection.
PA	(CHIR-) CHITRON SPA.	XX
XX	Masignani V, Mora M, Scarselli M;	PT Claim 27; Page 25; 78pp; English.
PT	WPI: 2003-120786/11.	XX
DR	DR-N-PSDB; ACP72989.	The present sequence comprises the protein sequence of the N2N3 region (amino acids 273-597) of the SdrG surface protein of coagulase-negative Staphylococcus epidermidis. A claimed antibody recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal antibody, including a chimeric, murine, humanized, human or single chain monoclonal antibody, which prevents a coagulase-negative staphylococcal infection in a human or animal by inhibiting binding of staphylococcal bacteria to fibrinogen. Such antibodies can be used to treat or prevent staphylococcal infections including nosocomial coagulase-negative staphylococcal infections in low birth weight infants. A claimed vaccine comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein.
XX	New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.	XX Sequence 343 AA;
XX	Claim 1; SEQ ID NO 1338; 49pp; English.	Query Match 13.1%; Score 133; DB 7; Length 343; Best Local Similarity 24.4%; Pred. No. 0.0037; Matches 54; Conservative 32; Mismatches 71; Indels 84; Gaps 9;
CC	The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and is a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention.	Qy 1 MRGSHHHHHHGGSQTP-----YTITNGTS-----QNTLSSLTF 33
CC	Sequence 96 AA;	Db 1 MRGSHHHHHHGGSLYRGSGNSVNHLLKVTQDQITEGYDDSDGJIKHDAENIYDVTIP 60
CC		Qy 34 NKNQISYKDIEWKTS----VLYFNRRGTSIDL-----EVDDRKTKSGDTMTVNIDKNTVPSDLTDSFAPIKIKDNSGEIIATGTYDNTN 111
CC		Db 61 -----R-L-S 66
CC		Qy 67 KQAKTQVHPNGTKRVRVDIKAGHTADLINTSDIKAIISVNVDTEKQVKDEKAANVQVBY 126
CC		Db 112 KQITP---FEDVYDREYNIKAHLKLTSYLDKSVP---NNNTKLQDVETKTAUSSVNKTI 165
CC		Qy 127 TITYNGTSQNILSNTF----KKNQIS-----YKDLENVNVSKVLKSNRGITDV 171
CC		Db 166 TVEYQPKPNEERTANLQSMTFTNDITKNTVETQTIYINPLRYSAKETVNYNISGNGDEGSTI 225
CC		Qy 172 D 172
CC		Db 226 D 226
CC		RESULT 15
DE	ABM79016 standard; protein; 343 AA.	RESULT 16
AC	ABM79016;	ABM79017
XX	15-JAN-2004 (first entry)	ID ABM79017 standard; protein; 316 AA.
DT	Staphylococcus epidermidis SdrG N2N3 domain.	XX
XX	KW	DE ABM79017;
XX	SdrG; surface protein; infection; antibacterial; vaccine.	XX DT 15-JAN-2004 (first entry)
OS	Staphylococcus epidermidis.	XX DE Staphylococcus epidermidis SdrG TR2 protein.
PN	W02003076470-A1.	XX KW SdrG; surface protein; infection; antibacterial; vaccine.
XX	18-SEP-2003.	XX OS Staphylococcus epidermidis.
PD		XX PN WO2003076470-A1.

				Location/Qualifiers
XX	PD	18-SEP-2003 .	XX	1. 17
XX	PP	05-MAR-2003 ; 2003WO-US006415.	XX	/note= "(His)6 tag and flexible linker peptide"
XX	PR	05-MAR-2003 ; 2002US-0361324P.	XX	16 . 391
XX	PA	(INHI-) INHIBITEX INC. (TEXA) UNIV TEXAS A & M SYSTEM.	XX	/note= "MSP-1(42)"
XX	PI	Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;	XX	
XX	PI	Robbins J, Vernachio J, Bowden MG;	XX	
XX	WPI	DR 2003-722324/68.	XX	
XX	PT	SdrG N1N2N3, SdrG N3 or SdrGTR2 useful for preparing a composition for treating or preventing a coagulase-negative staphylococcal infection.	XX	
XX	PT	PT 2003-722324/68.	XX	
XX	DR	DR 00626.	XX	
XX	DR	DR 2002-590798/63.	XX	
XX	PS	PT (REED-) REED ARMY INST RES WALTER.	XX	
XX	PS	PT Lyon JA, Angov E, Cohen JD, Voss G;	XX	
XX	PS	PT New vaccine comprising Plasmodium falciparum MSP-142 protein and an adjuvant, useful against malaria or for eliciting immune responses against P. falciparum.	XX	
XX	PS	PT Disclosure; Page 98-99; 99pp; English.	XX	
CC	CC	CC The present sequence is that of a recombinant protein comprising the Plasmodium falciparum 3D7 merozoite surface protein-1 42 kDa fragment (MSP-1(42)) with an N-terminal (His)6 tag and linker. Recombinant PSP-1(42) protein was produced as a soluble protein in Escherichia coli host cell cytoplasm by manipulation of IPTG concentration and induction temperature. MSP-1(42) was purified to greater than 95% purity, and showed immunoreactivity with anti-MSP-1 antibodies. It was stable when stored for 18 months at -80 degrees C. The invention relates to the production of large amounts of MSP-1(42) which maintain conformational epitopes critical for development of vaccines. The vaccines are useful against malaria or for eliciting immune responses against P. falciparum.	CC	
CC	CC	CC The recombinant MSP-1(42) proteins are useful in diagnostic assays, for in vitro monitoring of malaria infection or prognosis the response to treatment of malaria patients, and for production of antibodies used for malaria antigen detection or as therapeutic or prophylactic agents	CC	
XX	XX	XX Sequence 316 AA;	XX	
XX	XX	XX Query Match Score 131; DB 7; Length 316;	XX	
XX	XX	XX Best Local Similarity 22.6%; Pred. No. 0.0049;	XX	
XX	XX	XX Matches 53; Conservative 33; Mismatches 71; Indels 9;	XX	
Qy	1	1 MRGSHHHHHGGSQ----IPTITVNGTS-----ONLSSLTENKQQI 39	Db	
Db	1	1 MRGSHHHHHGGSQEQGSNVNHLLKVTDQSTITEGYDDSDGIIKAHDENLYDTVF---- 54	Qy	
Qy	40	40 SYKDIEVKVS---VLYFNRGISIDL-----RLSKOAKYT 72	Db	
Db	55	55 ---EVDKVKGSDTMTVNIDQNTVPSDLTDSFAIPKIKDNSEBIIATGTVDNTNKQITYT 111	Qy	
Qy	73	73 VHFKNQTRVVDLKGAGIHTADLINTSDIKAIISVNDTKQYDKEAKANVQPYITVNG 132	Db	
Db	112	112 --FTDVYDKVYENIKAHKLTKSYIDSKVP--NNNTKLDVEYKTAISVNTKTTEYKQ 165	Qy	
Qy	133	133 TSQNLTSNLTP-----KKNQIQS-----YKDLNEENYKSVLKNSNRGITDVD 172	Db	
Db	166	166 PNENRTANLQSMFTNIDTKHNTVEQTYINPLRYSAXETNVNISGNQDEGSTIID 220	Qy	
Qy	17	17 ABB79627 ABB79627 standard; protein; 391 AA.	Db	
XX	XX	XX RESULT 17 ABB79627 ABB79627 standard; protein; 391 AA.	XX	
XX	XX	XX ABB79627; 21-OCT-2002 (first entry)	XX	
XX	XX	XX Plasmodium falciparum MSP-1(42) recombinant protein.	XX	
XX	XX	XX Merozoite surface protein-1; MSP-1; malaria; vaccine; protozoacide.	XX	
XX	XX	XX Plasmodium falciparum.	XX	
OS	OS	OS Synthetic.	AC	
XX	XX	XX Chimeric.	XX	
RESULT 18	ABP71275		ID ABP71275 standard; protein; 391 AA.	
RESULT 19	ABP71275		ID ABP71275 standard; protein; 391 AA.	
RESULT 20	ABP71275		ID ABP71275 standard; protein; 391 AA.	
RESULT 21	ABP71275		ID ABP71275 standard; protein; 391 AA.	
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RESULT 198	ABP71275		ID ABP71275 standard; protein; 391 AA.	
RESULT 199				

XX	Key	FH	Location/Qualifiers	RESULT 21
	Peptide	PT	1. .12 /note= "vector pQE30-derived peptide"	ABU44119 standard; protein; 374 AA.
	PT	PT	13. .512 /note= "epitope M17"	
	Protein	FT		
	FT	FT		
	FT	FT		
XX	W09743314-A2.	XX		AC ABU44119;
PN		XX		XX DT 19-JUN-2003 (first entry)
PD	20-NOV-1997.	XX		DE Protein encoded by Prokaryotic essential gene #29646.
PP	14-MAY-1997;	XX		XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
PR	16-MAY-1996;	XX		XX OS Streptococcus mutans.
PA	(TEXA) UNIV TEXAS A & M SYSTEM. (UABR-) UAB RES FOUND.	XX		XX PN WO200277183-A2.
PA	XX	XX		XX PD 03-OCT-2002.
PI	Hoeoeak M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;	XX		XX PF 2002WO-US009107.
DR	WPI; 1998-008801/01.	XX		XX PR 21-MAR-2001; 2001US-00815242.
DR	N-PSDB; AT93438.	XX		PR 06-SEP-2001; 2001US-00948993.
PT	Antibody that interacts with collagen binding domain of Staphylococcal	XX		PR 25-OCT-2001; 2001US-0342923P.
PT	cna gene product - useful to prevent bacterial sepsis in animal infected	XX		PR 08-FEB-2002; 2002US-00072851.
PT	with Staphylococcus aureus.	XX		PR 06-MAR-2002; 2002US-0362699P.
PS	Claim 31; Page 117-119; 143pp; English.	XX		XX PA (ELIT-) ELITRA PHARM INC.
CC	This protein comprises Staphylococcus aureus collagen binding protein	XX		XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
CC	(CBP) epitope M55, i.e. amino acids 30-531 of full-length CBP, plus a	CC		PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
CC	vector-derived N-terminal peptide. Claimed 441, 849 and 1500 bp nucleic	CC		XX DR WPI; 2003-029926/02.
CC	acid sequences (see AT9436-38) respectively encode CBP epitopes M17,	CC		XX DR N-PSDB; ACA47989.
CC	M31 and M55 (see AA93155-54) that confer protection against S. aureus	CC		XX PT New antisense nucleic acids, useful for identifying proteins or screening
CC	infection. These nucleic acid sequences can be used in the recombinant	CC		PT for homologous nucleic acids required for cellular proliferation to
CC	production of the CBP epitopes. The CBP protein and antigenic epitopes	CC		PT isolate candidate molecules for rational drug discovery programs.
CC	are contemplated for use in the treatment of pathological infections,	CC		XX PS Claim 25; SEQ ID NO 72043; 1766pp; English.
CC	especially to prevent bacterial adhesion to collagen. The claimed nucleic	CC		XX PA The invention relates to an isolated nucleic acid comprising any one of
CC	acids as well as claimed anti-CBP antibodies will also be of use in	CC		CC the 6213 antisense sequences given in the specification where expression
CC	screening, diagnostic and therapeutic applications including active and	CC		CC of the nucleic acid inhibits proliferation of a cell. Also included are
CC	passive immunization and methods for the prevention of bacterial	CC		CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC	colonisation in an animal such as a human. The CBP epitopes are also	CC		CC encoding a polypeptide whose expression is inhibited by the antisense
CC	contemplated for use in the preparation of vaccines and as carrier	CC		CC polytide; (2) a host cell containing the vector; (3) an isolated
CC	proteins in vaccine formulations as well as in the formulation of	CC		CC polypeptide or its fragment whose expression is inhibited by the
CC	compositions for the prevention of S. aureus infection. (Updated on 25-	CC		CC antisense nucleic acid; (4) an antibody capable of specifically binding cellular
CC	MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS	CC		CC polytide; (5) producing the polypeptide; (6) inhibiting cellular
CC	field.)	XX		CC proliferation or the activity of a gene in an operon required for
SO	Sequence 512 AA:	XX		CC proliferation; (7) identifying a compound that influences the activity
Db	Query Match Score 11.5%; Length 512;	XX		CC of the gene product or that has an activity against a biological pathway
Matches 64; Best Local Similarity 23.8%; Pred. No. 0.17; Mismatches 29;	Score 11.5%; DB 2; Length 512;	XX		CC required for proliferation, or that inhibits cellular proliferation; (8)
Qy	1 MRGSHHHHHQSQIPPTITGNTSQLISSL-----LTP-NKQNQISYKD-----43	XX		CC identifying a gene required for cellular proliferation or the biological
Db	1 MRGSHHHHHQSARDSSST-NVTDLTVSPSKIEDGGKTTVKMFDKGKIQNGDMIKVA 59	XX		CC pathway in which a proliferation-required gene or its gene product lies
Qy	44 -----TENKVKS7-----LYFN--RGISDIDRLSKQAKYT 72	XX		CC or a gene on which the test compound that inhibits proliferation of an
Db	60 WPTSGTVKIEGYSKTVPLTVGEQVQAVITPDGATITNDKVEKLSDV----SGFAEFE 115	XX		CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
Qy	73 VHFKNCTKRVVDLKAGIHTADLINTSDIKASV---NVDTKVQVKDKEA-----118	XX		CC compound or culture comprising strains in which the gene
Db	116 VQGRNTQ-----TNTSDDKVATITSGNSKSTNTVVKSEAGTSSVFPYKKTG 161	XX		CC product is overexpressed or underexpressed; (11) determining the extent
Qy	119 ---KANVQVPTITGNTGTSNINLSNLTFKK---NQQISYKDLENN----KSVTKSNR 166	XX		CC to which each of the strains is present in a culture or collection of
Db	162 DMLPBTDTAVRMFLNNNERSVSKITDQIGQQQLDUSTLNINVGTNSNYSGQS 221	XX		CC strains; or (13) identifying the target of a compound that inhibits the
Qy	167 GITDVLRLSKQAKFTVNPKNFGTKWMDL 195	XX		CC proliferation of an organism. The antisense nucleic acids are useful for
Db	222 AITDPR-KAFPGSKVTV----DNTQTIDV 246	XX		CC cellular proliferation to isolate candidate molecules for rational
CC	CC drug discovery programs, or for screening homologous nucleic acids	CC		CC drug discovery programs, or for screening homologous nucleic acids
CC	CC required for proliferation in cells other than S. aureus, S. typhimurium	CC		CC or K. pneumoniae or P. aeruginosa. The present sequence is encoded by one
CC	CC the target prokaryotic essential genes. Note: The sequence data for this	CC		CC patent did not form part of the printed specification, but was obtained
CC	CC electronic format directly from WIPO int'l pub/published pct sequences	CC		CC ftp://wipo.int/pctdb/pctdb.html

XX	Sequence 374 AA;	CC production of antibodies used for malaria antigen detection or as therapeutic or prophylactic agents
SQ		CC
Query Match 11.3% ; Score 115; DB 6; Length 374;	XX	CC
Best Local Similarity 24.2% ; Pred. No. 0.15; Matches 52; Conservative 42; Mismatches 63; Indels 58; Gaps 13;	SQ	Sequence 393 AA;
Qy 18 ITVNGTSSNLLSSTFNNKNQQTSYKDIBNTKVKSVLQKAXTV 73		Query Match 11.3%; Score 114.5; DB 5; Length 393;
DB 131 ITVSGNKRAIESQI---EELGIKK-SDYLTLLFQANRFERNLSSKD-KWVKEAKLVY 184		Best Local Similarity 22.5%; Pred. No. 0.18; Matches 53; Conservative 34; Mismatches 90; Indels 59; Gaps 10;
Qy 74 HFNG-TKRVVD-----LKAGIHTADLINTSDIKA--ISVNVDTKKQVK 114		Matches 53; Conservatve 34; Mismatches 90; Indels 59; Gaps 10;
DB 185 HEPNHFTVRVKEYRIIAVQTDKGYPALENGTR-VOTVNASELPGSFVTINLDQEKEVR 243		Qy 4 SHHHHHH-GSQIP-YITINGTSQNSNILLTENKNQQISY-----KDIENKV 48
Qy 115 -----DKEAKANYQPVYITVNGTSSNLLTFFKRNQQTSYKDLENNVKSULKSN 165		Db 2 AHHHHHHPGGSIEGRGTMASISVMMNTLNSG--FENYDVYLKPLAGVYRSLSKQKIE--- 56
DB 244 ELVQKLADKSLKSLVGTSIVK--ISSVNSSTSKDOLLLLEMKD----NSVRVPL--- 289		Qy 49 KSVLAFNRGSDIDDLRLSKOAKTFTKRYVDLKAGIHTADLINTSDIKA-SVNVD 108
Qy 166 RGITDVDRRLSLSKOAKFTNFKNGTKVYIDLAGIY 200		Db 57 KNIFPNLNNDILNSRLKERRQFYFL-----DVLESILMQPKFHISSEMYIE 102
DB 290 ---SEIDDKLPLVYSKIKKNLTDGS--1VDMEVGIV 319		Qy 109 TTKQYDKEAKARYQPVYITVNGTSSNLI--LSNLTFKRNQQTSYKDLENNVKSULKSN 165
Qy 222 ABB79625 standard; protein; 393 AA.		Db 103 DSFRKLNSBQNTLKSQKVIKESVENDIKFAQBGSISYEKVLAKYKDDLESIKRKVKEE 162
ID ABB79625		Qy 166 R-----GITYDVLRLSKQAKETVN---FRNGTKKVV---IDLKAGI 199
XX ABB79625		Db 163 KEKFPSSSPPTPPSSPAKTDQEKCSKFLPFLTNIEFLYNNLVNKDDYLINLKARI 218
AC ABB79625;		RESULT 2.3
XX DT 21-OCT-2002 (first entry)		ABP71273
XX DE E. coli expressed P. falciparum MSP-1 recombinant protein.		ID ABP71273 standard; protein; 393 AA.
XX KW Merozoite surface protein-1; MSP-1; malaria; vaccine; protozoacide.		XX AC ABP71273;
XX OS Plasmodium falciparum.		XX DT 28-APR-2003 (first entry)
OS Synthetic.		XX P. falciparum MSP1_42 (3D7) protein sequence in clone PET42A.
OS Chimeric.		XX KW MSP-1_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.
OS PN WO2003004525-A2.		XX OS Plasmodium falciparum.
XX PD 01-AUG-2002.		XX XX WO2003004525-A2.
XX PP 25-JAN-2002; 2002WO-US002554.		XX XX 16-JAN-2003.
XX PR 26-JAN-2001; 2001US-0264535P.		XX PF 25-JAN-2002; 2002WO-US002428.
XX PA (REED-) REED ARMY INST RES WALTER.		XX PR 29-JAN-2001; 2001US-0264535P.
XX PI Lyon JA, Argov E, Cohen JD, Voss G,		XX PR 26-OCT-2001; 2001US-0341564P.
XX DR 2002-590798/63.		XX PA (REED-) REED ARMY INST RES WALTER.
XX Disclosure; Page 92-93; 99pp; English.		XX XX Lyon JA, Argov E;
XX The present sequence is that of a recombinant protein comprising		XX DR WPI; 2003-221577/21.
CC Plasmodium falciparum 3D7 merozoite surface protein-1 42 kDa fragment		XX PT New recombinant Plasmodium falciparum merozoite protein (MSP)-1-42 which retains its native folding. The protein is useful for detecting and preventing malaria infection, and for antibody production.
CC (MSP-1(42)) with an N-terminal (His)6-tag for affinity purification and 3 linker amino acids. The levels of expression of the recombinant protein, encoded by plasmid pET-IEGR-42 (AT), were 2-5% of total E. coli protein,		XX PS Disclosure; Page 96-97; 104pp; English.
CC and the protein was correctly folded based on immunoreactivity with a series of MSP-1(19) specific monoclonal antibodies. The present invention relates to the production of large amounts of MSP-1(42) which maintain conformational epitopes critical for development of vaccines. The		XX CC The invention relates to a recombinant Plasmodium falciparum merozoite protein, (MSP)-1-42 which retains its native folding. The protein is useful as a diagnostic reagent, in antibody production, and as a vaccine against malaria. The antibody may also be used for detecting and treating chronic malaria infection. The present sequence represents a recombinant B. coli expressed P. falciparum MAP-1_42 protein expressed in clone pET42A
CC vaccines are useful against malaria or for eliciting immune responses		XX SQ Sequence 393 AA;
CC against P. falciparum. The recombinant MSP-1(42) proteins are useful in		Query Match 11.3%; Score 114.5; DB 6; Length 393;
CC diagnostic assays, for in vitro monitoring of malaria infection or		Best Local Similarity 22.5%; Pred. No. 0.18;
CC prognosing the response to treatment of malaria patients, and for		

of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation or to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Sequence 10-11.						
	Query	Match	Score	Length	DB	
Best Local Matches	44;	Similarity	22.0%	DB 6;	Length 246;	
Matches	44;	Conservative	40;	Pred. No. 0.12;	Mismatches 65;	Indels 51;
					Gaps 10	
Dy	23	TSQNLSSLTENKNGQI	--SYKDIPNKKVSVLYFNRGIDIDLRSQAKYTVPFKNGT	79		
Db	49	TKSNMKEELNTNLNENIFATYNFKDMNK	--LIGNPYTIEVEIKRLPKNLIISKE--	102		
Dy	80	KRV-	--VDLKAGIHTADLINTSDIA	122	--ISVNNDTKQVKQVKREAKANV	122
Db	103	KEIFAVLKDEDDNYCDKKGKL	-LEERGSNESKQDLDIVDYSIDDNKSUKFKRYK	--	158	
Dy	123	QVPTTITVNGTSQNLTSNLTKKGQ	--QISYKDL--ENNVKSVLKSNRQGITDDYDLRLS	176		
Db	159	--	--TKENVFKTNLVLRGEIYRKINYVNLKCESNIEMLTRSN	--	--IKILLS	203
Dy	177	KQAKFTYNEKGITKVKIDLK	196			
Db	204	NNDDLDYNISRVSKLIDLQ		223		
RESULT 27						
ID	ABU33173	standard; protein	963 AA.			
XX	ABU33173;					
XX	19-JUN-2003	(first entry)				
XX	Protein encoded by Prokaryotic essential gene #18700.					
XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.					
XX	Legionella pneumophila.					
DS	WO200277183-A2.					
XX	03-OCT-2002.					
XX	21-MAR-2002; 2002WO-US009107.					
PP						

PD 13-NOV-2003.
 XX
 PF 25-MAR-2003; 2003WO-DK000198.
 XX
 PR 10-APR-2002; 2002DK-00000534.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen JT, Jorgensen ST, Rasmussen MD, Olsen PR, Clausen IG;
 XX
 DR WPI; 2004-053045/05.
 DR N-PSDB; ADG32047.
 XX
 PR New mutant *Bacillus licheniformis* host cell secreting 5 % less of one or
 PR more secreted polypeptides than the parent host cell, useful for
 PR producing a product of interest e.g. polypeptides, amino acids or
 PR carbohydrates.
 XX
 PS Claim 1; SEQ ID NO 18; 422pp; English.
 CC This invention relates to a novel *Bacillus licheniformis* (*B.*
licheniformis) mutant host cell derived from a parent *B. licheniformis*
 CC host cell that is mutated in genes encoding secreted polypeptides.
 CC Specifically, it refers to the generation of an improved *Bacillus* host
 CC that reduces the need for product purification caused by contaminant
 CC secreted native polypeptides in the culture medium. Accordingly, the
 CC present invention describes reducing the expression of these native
 CC proteins (e.g. proteolytic enzymes, nutrient uptake factors and signal
 CC molecules), which in turn makes it easier to purify the heterologous
 CC product of interest and therefore improving the production process.
 CC Further benefits of a mutated host cell include an increase in total
 CC product yield and a longevity of shelf life attributable to improved
 CC product stability and purity. This polypeptide is a mutant *B.*
 CC *licheniformis* secreted polypeptide of the invention.
 SQ Sequence 438 AA;

Query Match	Score 110; DB 8; Length 438;
Best Local Similarity	19.7%; Prod. No. 0.52;
Matches 50; Conservative	36; Mismatches 86; Indels 82; Gaps 7;
Qy 24	SQNLISSUFENQQISYKDIENKVK-----SVLYFNR-----
Db 115	ARNVADGLTLTINPSTVTTIEKTKTEFPVEVDINKNKKMDGYTPELPINPKVNST 174
Qy 57	-----GSDIDURLSKQVKDKERAKANTQV-PYITVGTGTSQNLNSLTPKKNQQISY-----
Db 175	GSKAVIDNIQKATINEGDVTVERAKLTVYDKDGVNLVEVSPPVKITVPVTPSPS 234
Qy 101	KAI SVNNVDTKKQVKDKERAKANTQV-PYITVGTGTSQNLNSLTPKKNQQISY-----
Db 235	KKLPVKVNRKGSLPDGTSISSLDISPGEVTVYG-PQNVLDSLEFVADEILSKLKDDE 293
Qy 152	-----KDLENNPKVSLRSNRGRTIDV-DLRL-SKOAKFT 182
Db 294	LEAGIKVDPGAKKVSPEKVKIKVVDKEEKKLNQSIKTAGLNDSRDLEFDPKSGKLD 353
Qy 183	VNFQNGTKVQDJK 196
Db 354	ITAKGSTTAIEKLQ 367

Query Match 10.8%; Score 110; DB 3; Length 1095;
 Best Local Similarity 25.1%; Pred. No. 1.8;
 Matches 50; Conservative 29; Mismatches 76; Indels 44; Gaps 8;

RESULT 30
 APB01835 standard; protein; 1095 AA.
 XX
 AC APB01835;
 XX
 DT 12-SEP-2003 (revised)
 DT 11-SEP-2000 (first entry)
 XX Haemophilus influenzae strain LCDC2 mature HMW1A protein, SEQ ID NO:45.
 DE

Mature HMW protein; hmw gene; hmwA1; hmwA2; high molecular weight;
 KW non-typeable Haemophilus influenzae; NTHi; non-encapsulated;
 KW recombinant production; Escherichia coli; antibacterial; vaccine;
 KW human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
 KW detection; diagnosis.
 XX OS Haemophilus influenzae; strain LCDC2.
 XX WO200020609-A2.
 XX WPI; 2000-303789/26.
 DR N-PSDB; AAA52184.
 XX
 PR 07-OCT-1999; 99WO-CA000938.
 PR 07-OCT-1998; 98US-00167568.
 PR 08-DEC-1998; 98US-00206942.
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX PI Loosmore SM, Yang Y, Klein MH;
 XX WPI; Fig 22A-P; 307pp; English.
 XX
 The invention relates to the recombinant production of Haemophilus
 CC influenzae high molecular weight (HMW) proteins in *Escherichia coli*. The
 CC expression construct used to effect recombinant expression comprises a
 CC promoter functional in *E. coli* (e.g., the T7 promoter) operably linked to
 CC a modified hmwABC operon from a non-typeable (non-encapsulated) *H.*
 CC influenzae (NTHi). Most HMW-expressing NTHi strains contain two hmw gene
 CC clusters termed hmw1ABC and hmw2ABC. Each hmwABC operon comprises hmwA,
 CC hmwb and hmwc genes encode the structural HMW proteins
 CC and the hmwb and hmwc genes encode accessory proteins which are
 CC responsible for post-translational processing and secretion of the HMW
 CC proteins. The modified hmwABC operon used in the expression construct of
 CC the invention contains an A gene modified such that it encodes only the
 CC mature HMW. The invention also discloses hmw genes (AAA2175-A52198)
 CC and HMW proteins (AAB01824-B0189) from the non-typeable *H. influenzae*
 CC strains Joyce, K1, K21, LCDC2, PMHi, 15 and 12. The nucleic acids and
 CC vectors are used for the production of recombinant *H. influenzae* HMW
 CC proteins which can be used as vaccines to mediate a humoral or cell-
 CC mediated immune response to provide protection against diseases in humans
 CC caused by *H. influenzae* (e.g., otitis media, epiglottitis, pneumonia and
 CC tracheobronchitis). The HMW proteins are also useful as antigens in
 CC immunoassays for detecting antibodies against Haemophilus HMW proteins
 CC and/or HMW peptides. The nucleotide sequences encoding the HMW proteins
 CC can be used to isolate and clone hmw genes from other non-typeable
 CC strains of Haemophilus via hybridization reactions. The present sequence
 CC represents a mature HMW protein from a non-typeable strain of *H.*
 CC influenzae. (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 1095 AA;

Query Match 10.8%; Score 110; DB 3; Length 1095;
 Best Local Similarity 25.1%; Pred. No. 1.8;
 Matches 50; Conservative 29; Mismatches 76; Indels 44; Gaps 8;

Qy 18 ITVNQIYKTDIENKVSVLYFNRGISDIDLRSKQARY 71
 Db 446 LIVTSAINERLNLVEGSAFKFLANPNYSN-----VSGGLFDNQGKSNISI----AKG 494
 Qy 72 TVHFK- -NGTKRKYVVDLKGHTADLINTSD-----IKAI SVNNVDTKKQVKDKERAKANTQV 123
 Db 495 GAHPFDINNTK-----SINTTNSDSAYTITBENITNSNGDUNITDNKNAEIQ 544
 Qy 124 VPYTI-----TYNGTSONILSNTLFKK---NQQISYKDLNNNTKSVLKSNRGITDVDLR 174

Db	545 IGGNISQEGNLTISDXKINITNQITIKGVNREDSSTANNANLTIKTKEBLQLTCQLDN 604	CC (Updated on 12-SEP-2003 to standardise OS field)
Qy	175 LSKQAKPTVNPNGTKKVI 193	XX SQ Sequence 1101 AA;
Db	605 ISGFDKAETAKEGADLII 623	Query Match 10.8%; Score 110; DB 3; Length 1101; Best Local Similarity 25.1%; Pred. No. 1.8; Matches 50; Conservative 29; Mismatches 76; Indels 44; Gaps 8;
RESULT 31		
AAB01834		
ID AAB01834	standard; protein; 1101 AA.	Qy 18 ITVGTSQNISSLT-----FKNQOISYKDIENKVSKVLYFNRGISDIDILRLSKOAKY 71
XX		Db 452 LTVTGSAINIEKNLTVEGSAFLANPNSFN-----VGGLFDNQSKSNISI----AKG 500
AC AAB01834;		Qy 72 TVHFK--NGTKRVRVDLKGAIHTADLINTSD----IAKISVNVDTKQVKDKEAKANVQ 123
XX	12-SEP-2003 (revised)	Db 501 GAHFRDINNTK-----SLNLTNSDSAYRTTIEGNITNSGDLNLTDNKNAEIQ 550
DT 11-SEP-2000 (first entry)		XX
DB Haemophilus influenzae strain LCDC2 HMW1A protein, SEQ ID NO:43.	Qy 124 VPYTI-----TVNGTQNILLNLTFKK--NQQISYKDKLENNVKSVLKSNRGITDVDR 174	
XX		Db 551 IGGNISQEGNLTISDXKINITNQITIKGVNKEIDSSTANNANLTIKTRELQLTGDLN 610
KW HMW protein; hmw gene; hmwA1; hmwA2; high molecular weight;	Qy 175 LSKQAKPTVNPNGTKKVI 193	XX
KW non-typeable Haemophilus influenzae (NTHi); non-encapsulated;	Db 611 ISGFDKAETAKEGADLII 629	XX
KW recombinant production; Escherichia coli; antibacterial; vaccine;		RESULT 32
KW human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;		AAB01825
KW detection; diagnosis.		ID AAB01825 standard; protein; 1221 AA.
XX	OS Haemophilus influenzae; strain LCDC2.	XX
PN WO2000020609-A2.		AC AAB01825;
XX		XX DT 12-SEP-2003 (revised)
PD 13-APR-2000.		DT 11-SEP-2000 (first entry)
XX	PP 07-OCT-1999; 99WO-CA0000938.	XX Haemophilus influenzae strain Joyce mature HMW1A protein, SEQ ID NO:28.
XX	PR 07-OCT-1998; 98US-00167568.	XX
PR 08-DEC-1998; 98US-00206942.		KW Nature HMW protein; hmw gene; hmwA1; hmwA2; high molecular weight;
XX	(CONN-) CONNAUGHT LAB LTD.	XX KW non-typeable Haemophilus influenzae; NTHi; non-encapsulated;
XX	PI Loosmore SM, Yang Y, Klein MH;	XX KW recombinant production; Escherichia coli; antibacterial; vaccine;
XX	DR; 2000-303789/26.	XX KW human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
XX	Nucleic acid molecule for producing recombinant high molecular weight	XX KW detection; diagnosis.
PT proteins of Haemophilus which are used as a vaccine to provide protection		XX
PT against Haemophilus induced diseases in humans.		OS Haemophilus influenzae; strain Joyce.
XX		XX PN WO2000020609-A2.
PS Claim 12; FIG 22A-P; 307pp; English.		XX PD 13-APR-2000.
XX	The invention relates to the recombinant production of Haemophilus	XX XX
CC influenzae high molecular weight (HMW) proteins in Escherichia coli. The		XX PP 07-OCT-1999; 99WO-CA0000938.
CC expression construct used to effect recombinant expression comprises a		CC PR 07-OCT-1998; 98US-00167568.
CC promoter functional in E. coli (e.g., the T7 promoter) operably linked to		CC PR 08-DEC-1998; 98US-00206942.
CC a modified hmwABC operon from a non-typeable (non-encapsulated) H.		XX (CONN-) CONNAUGHT LAB LTD.
CC influenzae (NTHi). Most HMW-expressing NTHi strains contain two hmw gene		XX PI Loosmore SM, Yang Y, Klein MH;
CC clusters termed hmwABC and hmw2ABC. Each hmwABC operon comprises hmwA,		XX WPI; 2000-303789/26.
CC hmwB and hmwC genes. The hmwA genes encode the structural HMW proteins		DR N-PSDB; AAA52176.
CC and the hmwB and hmwC genes encode accessory proteins which are		XX PT Nucleic acid molecule for producing recombinant high molecular weight
CC responsible for post-translational processing and secretion of the HMW		CC PT proteins of Haemophilus which are used as a vaccine to provide protection
CC proteins. The modified hmwABC operon used in the expression construct of		CC PT against Haemophilus induced diseases in humans.
CC the invention contains an A gene modified such that it encodes only the		XX PS Claim 8; Fig 18A-R; 307pp; English.
CC mature HMW. The invention also discloses hmwA genes (AAA52175-AA52198)		XX
CC and HMW proteins (AAB01824-B01849) from the non-typeable H. influenzae		CC
CC strains Joyce, K1, K21, LCDC2, PMHL 15 and 12. The nucleic acids and		CC
CC vectors are used for the production of recombinant H. influenzae HM		CC
CC proteins which can be used as vaccines to mediate a humoral or cell-		CC
CC mediated immune response to provide protection against diseases in humans		CC
CC caused by H. influenzae (e.g., otitis media, epiglottitis, pneumonia and		CC
CC tracheobronchitis). The HMW proteins are also used as antigens in		CC
CC immunoassays for detecting antibodies against Haemophilus HMW proteins		CC
CC and HMW peptides. The nucleic acid sequences encoding the HMW proteins		CC
CC can be used to isolate and clone hmw genes from other non-typeable		CC
CC strains of Haemophilus via hybridisation reactions. The present sequence		CC
CC represents an HMWA protein from a non-typeable strain of H. influenzae.		CC

hmwB and hmwC genes. The hmwA genes encode the structural HmWA proteins and the hmwB and hmwC genes encode accessory proteins which are responsible for post-translational processing and secretion of the HmWA proteins. The modified hmwABC operon used in the expression construct of the invention contains an A gene modified such that it encodes only the mature HmWA. The invention also discloses hmwA genes (AAA2175-A5218) and HmWA proteins (AB01824-B01849) from the non-typeable *H. influenzae* strains Joyc, K1, K21, LCDC2, PMH1, 15 and 12. The nucleic acids and vectors are used for the production of recombinant *H. influenzae* HMW proteins which can be used as vaccines to mediate a humoral or cell-mediated immune response to provide protection against diseases in humans caused by *H. influenzae* (e.g., otitis media, epiglottitis, pneumonia and tracheobronchitis). The HMW proteins are also useful as antigens in immunoassays for detecting antibodies against Haemophilus. HMW proteins and/or HMW peptides. The nucleotide sequences encoding the HMW proteins can be used to isolate and clone HMW genes from other non-typeable strains of *Haemophilus* via hybridisation reactions. The present sequence represents a mature HMWA protein from a non-typeable strain of *H. influenzae*. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 1221 AA;

Query Match	10.8%	Score 110;	DB 3;	Length 1221;
Best Local Similarity	23.7%;	Pred. No. 2.1;		
Matches	54;	Conservative	28;	Mismatches 82; Indels 64; Gaps 9;
Qy	3	GSHHHHHGGSQIPYTI-----TVRGTSONIILSCLTFENQNQISQYKDIENKVSKV	51	
Db	422	GSDFDNH--QKPLTIKKDVIINSGNLTAGVNININGNLTVNNGANL--KAITNFTENV	476	
Qy	52	-LYFNRGISIDDLRLSKQAKYTIVHFRKGTRVVDLKAGHTADLINTSDIKAIKVNVDT	109	
Db	477	GGLFDNGNGNSNTI-----ARGAKPFDKNTSSSN-TITNSDT	514	
Qy	110	KKQ-----VKDEKAKAVYQPYTI-----TVNGTSONIILSNLTFKK--	145	
Db	515	TYRTTIEGGNITNKGDNIIIDNKGNAEQIGGNISOKEGNLTISDKDKNITNQITIKGV	574	
Qy	146	NQOISYKDLLENNVKVKSNSNCGTIDVPLRSQAKETVNPNGTKKVI	193	
Db	575	NKEDSDSSSTANNANLTIKTKELQLTGPNLNISGFDKAEITAKEGADLU	622	

Locsmore SM, Yang Y, Klein MH;

XX WP1; 2000-303789/26.

DR N-PSDB; AAA52175.

XX PT Nucleic acid molecule for producing recombinant high molecular weight PT proteins of Haemophilus which are used as a vaccine to provide protection PT against Haemophilus induced diseases in humans.

XX PS Claim 12; Fig 18A-R; 307pp; English.

The invention relates to the recombinant production of Haemophilus influenzae high molecular weight (HMW) proteins in *Escherichia coli*. The expression construct used to effect recombinant expression comprises a promoter functional in *E. coli* (e.g., the T7 promoter) operably linked to a modified hmwABC operon from a non-typeable (non-encapsulated) *H. influenzae* (NTHi). Most HMW strains contain two hmw gene clusters termed hmwlABC and hmw2ABC. Each hmwABC operon comprises hmwa, hmwb and hmwc genes. The hmwa genes encode the structural HMWA proteins and the hmwb and hmwc genes encode accessory proteins which are responsible for post-translational processing and secretion of the HMWA proteins. The modified hmwABC operon used in the expression construct of the invention contains an A gene modified such that it encodes only the mature HMWA. The invention also discloses hmwa genes (AAAS2175-A5218) and HMWA proteins (AB01824-B01849) from the non-typeable *H. influenzae* strains Joyc, K1, K21, LCDC2, PMH1, 15 and 12. The nucleic acids and vectors are used for the production of recombinant *H. influenzae* HMW proteins which can be used as vaccines to mediate a humoral or cell-mediated immune response to provide protection against diseases in humans caused by *H. influenzae* (e.g., otitis media, epiglottitis, pneumonia and tracheobronchitis). The HMW proteins are also useful as antigens in immunoassays for detecting antibodies against Haemophilus. HMW proteins and/or HMW peptides. The nucleotide sequences encoding the HMW proteins can be used to isolate and clone HMW genes from other non-typeable strains of *Haemophilus* via hybridisation reactions. The present sequence represents an HMWA protein from a non-typeable strain of *H. influenzae*. (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 1227 AA;

Query Match	10.8%;	Score 110;	DB 3;	Length 1227;
Best Local Similarity	23.7%;	Pred. No. 2.1;		
Matches	54;	Conservative	28;	Mismatches 82; Indels 64; Gaps 9;
Qy	3	GSHHHHHHGGSQIPYTI-----TVNGTSONIILSSLTENQNQISQYKDIENKVSKV	51	
Db	428	GSDFDNH--QKPLTIKKDVIINSGNLTAGVNININGNLTVNNGANL--KAITNFTENV	482	
Qy	52	--LYFNRGISIDDLRLSKQAKYTIVHFRKGTRVVDLKAGHTADLINTSDIKAIKVNVDT	109	
Db	483	GGLFDNGNGNSNTI-----ARGAKPFDKNTSSSN-TITNSDT	520	
Qy	110	KKQ-----VKDEKAKAVYQPYTI-----TVNGTSONIILSNLTFKK--	145	
Db	521	TYRTTIEGGNITNKGDNIIIDNKGNAEQIGGNISOKEGNLTISDKDKNITNQITIKGV	580	
Qy	146	NQOISYKDLLENNVKVKSNSNCGTIDVPLRSQAKETVNPNGTKKVI	193	
Db	581	NKEDSDSSSTANNANLTIKTKELQLTGPNLNISGFDKAEITAKEGADLU	628	

XX SQ Sequence 1227 AA;

Query Match 10.8%; Score 110; DB 3; Length 1227;

Best Local Similarity 23.7%; Pred. No. 2.1;

Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

Qy 3 GSHHHHHHGGSQIPYTI-----TVNGTSONIILSSLTENQNQISQYKDIENKVSKV

51

Db 428 GSDFDNH--QKPLTIKKDVIINSGNLTAGVNININGNLTVNNGANL--KAITNFTENV

482

Qy 52 --LYFNRGISIDDLRLSKQAKYTIVHFRKGTRVVDLKAGHTADLINTSDIKAIKVNVDT

109

Db 483 GGLFDNGNGNSNTI-----ARGAKPFDKNTSSSN-TITNSDT

520

Qy 110 KKQ-----VKDEKAKAVYQPYTI-----TVNGTSONIILSNLTFKK--

145

Db 521 TYRTTIEGGNITNKGDNIIIDNKGNAEQIGGNISOKEGNLTISDKDKNITNQITIKGV

580

Qy 146 NQOISYKDLLENNVKVKSNSNCGTIDVPLRSQAKETVNPNGTKKVI

193

Db 581 NKEDSDSSSTANNANLTIKTKELQLTGPNLNISGFDKAEITAKEGADLU

628

XX

RESULT 3:4

ABP39160 standard; protein; 288 AA.

XX ABP39160;

AC 24-JUL-2002 (first entry)

XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4005.

XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

KW antibacterial; gene therapy.

(CONN) CONNAUGHT LAB LTD.

XX

CC prodn. of antimalarial vaccines. See also AAQ13727-8

XX Sequence 493 AA;

Query Match Score 107.5; DB 2; Length 493;

Best Local Similarity 25.4%; Pred. No. 1;

Matches 50; Conservative 24; Mismatches 72; Indels 51; Gaps 9;

Qy 1 MRGSHHHHHGGQIPTITUNGTSQ--NILSLLTENKQQISYKDENKVSKVLYNPGI 58

Db 1 MRGSHHHHHGGQIPTITUNGTSQ--VNSVNKENMNKVNNAVKINAQDKVNAVKNSVNKLNVV 52

Qy 59 SDIDLRSKQAKY---TVHFNGTKRVVDLKGAGIPTADLINTSDIKAISSVNVDTKEQVKD 115

Db 53 NKTNVLSKLNAVYKVNSVHKNNAVKY---NAVNVKNAVNV---KAVNVNKEDILN 101

Qy 116 KEAKANQVQPVPTITVNGTSQNLNLTKKNNQISYKDENNVKSVLKSNRGITDVDLLR 175

Db 102 K-----LNALYKOMAVYKOMAL-NKVSAVNVK---VSAVNKVS 134

Qy 176 SKQAKPTVNPNGTKKV 192

Db 135 AVNKGAVNRYVNGVNVK 151

RESULT 38

ID AAW31555 standard; protein; 345 AA.

XX AAW31555;

XX 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 21-MAY-1998 (first entry)

XX DB Fibronectin-binding MSCRAMM derivative pCP33.

XX KW Fibronectin; pCP33; collagen binding protein; sepsis; infection;

XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;

XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

XX PT 1_12 /note= "vector pQE30-derived peptide"

XX PN WO9743314-A2.

XX PD 20-NOV-1997.

XX PP 14-MAY-1997; 97WO-US0008210.

XX PR 16-MAY-1996; 96US-0017678P.

XX PA (TEXA) UNIV TEXAS A & M SYSTEM.

PA (UAB-) UAB RES FOUND.

XX PI Hoeoeck M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

XX XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

XX cna gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding

XX microbial surface component recognising adhesive matrix molecule (MSCRAMM)

XX derivative pCP33, plus a vector-derived N-terminal peptide. The invention

XX relates to claimed nucleic acid sequences (see AAT93416-38) encoding S.

XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see

CC AAW31552-54) that confer protection against *S. aureus* infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and is carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of *S. aureus*
 CC infection. pCP33 and PQD (see AAW31556) were used to raise anti-NSCRAAM
 CC polyclonal antibodies used in passive immunization against bovine
 CC mastitis. (Updated on 27-
 CC AUG-2003 to correct OS Field.) (Updated on 27-
 XX AUG-2003 to correct OS Field.)

Sequence 345 AA;

Query	Match	Score 106;	DB 2;	Length 345;
	Best Local Similarity	23.3%;	Pred. No. 0.83;	Gaps 11;
	Matches	35;	Mismatches	90; Indels 46;
	Matche	52;	Conservative	
Qy	1 MRGSHHHHHGGQIPTITUNGTSQ--NILSLLTENKQQISYKDENKVSKVLYNPGI 58	Qy	1 MRGSHHHHHGGQIPTITUNGTSQ--NILSLLTENKQQISYKDENKVSKVLYNPGI--N 55	Db 1 MRGSHHHHHGGQIPTITUNGTSQ--NILSLLTENKQQISYKDENKVSKVLYNPGI 60
Db	1 MRGSHHHHHGGQIPTITUNGTSQ--VNSVNKENMNKVNNAVKINAQDKVNAVKNSVNKLNVV 52	Db	1 MRGSHHHHHGGQIPTITUNGTSQ--VNSVNKENMNKVNNAVKINAQDKVNAVKNSVNKLNVV 52	XX
Qy	59 SDIDLRSKQAKY---TVHFNGTKRVVDLKGAGIPTADLINTSDIKAISSVNVDTKEQVKD 115	Qy	56 RGISDIDLRSKQAKYTVHFNGTKRVVDLKGAG-----IHT ADLINT-S 98	XX
Db	53 NKTNVLSKLNAVYKVNSVHKNNAVKY---NAVNVKNAVNV---KAVNVNKEDILN 101	Db	61 SAVKGDTFKITVPKELNNGTSTAKVPPIMAGDQVLANGVTDGSGTIVYPTDGVNTKQD 120	XX
Qy	116 KEAKANQVQPVPTITVNGTSQNLNLTKKNNQISYKDENNVKSVLKSNRGITDV DLLR 175	Qy	99 DIKAI-----SYNDTQQVQKDKEAKANVQVP-----YIITVNGTSQNI 137	XX
Db	102 K-----LNALYKOMAVYKOMAL-NKVSAVNVK---VSAVNKVS 134	Db	121 DVKAUTMPAYIDPENVKCTGNVLTATGIGSTANKTVLVDLRSKQ 180	XX
Qy	176 SKQAKPTVNPNGTKKV 192	Db	138 -LSNLTFKKGQNOISYKDENNVKSVLKSN-RGITDVDLRSKQ 178	XX
Db	135 AVNKGAVNRYVNGVNVK 151	Db	161 DKTNNTYRQI1YVNPNSG-DNVIYAPVLTGNLKPNTDSNALDQ 222	XX

RESULT 39

ABM79015

ID ABM79015 standard; protein; 560 AA.

XX AC ABM79015;

XX DT 15-JUN-2004 (first entry)

XX DB Staphylococcus epidermidis Sdrg N1N2N3 domain.

XX KW surface protein; infection; antibacterial; vaccine.

XX OS Staphylococcus epidermidis.

XX OS WO2003076470-A1.

XX PD 18-SEP-2003.

XX PP 05-MAR-2003; 2003WO-US006415.

XX PR 05-MAR-2002; 2002US-0361324P.

XX XX (INHIBITEX INC. (TEVA) UNIV TEXAS A & M SYSTEM.

XX PA PI Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hock M;

XX PI PI Robbins J, Vernachio J, Bowden MG;

XX DR WPI; 2003-722324/68.

XX PT New antibody recognizing a *Staphylococcus epidermidis* protein comprising
 CC Sdrg N1N2N3, Scrg N2N3 or ScdcrTR2 useful for preparing a composition for
 CC treating or preventing a coagulase-negative staphylococcal infection.
 CC Claim 27; Page 24-25; 78pp; English.
 CC The present sequence comprises the protein sequence of the N1N2N3 region
 CC (amino acids 50-597), or putative A domain, of the Sdrg surface protein

of coagulase-negative *Staphylococcus epidermidis*. A claimed antibody recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal antibody, including a chimeric, murine, humanized, human or single chain monoclonal antibody, which prevents a coagulase-negative staphylococcal infection in a human or animal by inhibiting binding of staphylococcal bacteria to fibrogen. Such antibodies can be used to treat or prevent staphylococcal infections including nosocomial coagulase-negative staphylococcal infections in low birth weight infants. A claimed vaccine comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein.

XX Sequence 560 AA;

Query Match Score 105; DB 7; Length 560;
Best Local Similarity 24.6%; Pred. No. 2; Mismatches 41; Indels 76; Gaps 7;

Matches 44; Conservative 18; CC

Qy 1 MRGSHHHHGGSOIPIYTIVNGTSQNLISSLTFNKNQQISYKDIENKVSKVLYFNRG-1 58

Db 1 MRGSHHHHGGSE-----ENTDVQTKDSNMDEL 29

Qy 59 SPIDLRLSKQAKYTQVHFNGTTRVVDLKAGIHTADLINTSDIKAIISVNVDTKQVKDKEA 118

Db 30 SDSNDQSSNEEK-----NDVINSQ---SINTDDNQIKKEET 64

Qy 119 KANQVQPVITTYNGTSQNLSNIT-----FKEHQIQISKYDLENNVVK--SVLKSIN 165

Db 65 NSN-----DATENRSKDITQSTTINVQDNEATFLQKTPQDNTQLKEEVREBPSVSESSN 117

RESULT 40
ID ADP25447 standard; protein: 1781 AA.
XX

AC ADP25447;

CC

DN 09-SEP-2004 (first entry)

XX Plasmodium falciparum antigen amino acid sequence SEQ ID NO:24.

XX Plasmodium falciparum; malaria parasite; antigen; malaria; immunogenic; immune response; cytostatic; anti-HIV; virucide; hepatotropic; antibacterial; vaccine; cancer; infectious disease; AIDS; hepatitis; bacterial infection.

XX Plasmodium falciparum.

XX WO2004053086-A2.

XX PD 24-JUN-2004.

XX PP 08-DEC-2003; 2003WO-US038986.

XX PR 06-DEC-2002; 2002US-0431494P.

XX PA (EPIMMUNE INC.
(USNA) US SEC OF NAVY.

XX PI Doolan DL; Carucci DJ, Sidney J, Southwood S;

XX DR 2004-468856/44.

XX New isolated and/or purified Plasmodium falciparum polynucleotide sequences, useful in inducing an immune response for preventing and/or treating cancer and infectious diseases, such as AIDS, hepatitis, and bacterial infections.

XX Claim 22; SEQ ID NO 24; 253pp; English.

XX The present invention describes an isolated and/or purified Plasmodium falciparum (malaria parasite) antigen polynucleotide sequence, encoding an immunogenic peptide. Also described: (1) a primer or detection probe for hybridisation with a target sequence or the amplicon generated from a

target sequence comprising a sequence of at least 8-30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 consecutive nucleotides of any of the polynucleotide sequences as described above; (2) a DNA chip comprising any of the polynucleotide sequences described above; (3) a vector comprising a promoter operably linked to any of the nucleic acid sequences described above; (4) a host cell transformed by the vector of (3) or the polynucleotide described above; (5) a composition comprising a carrier and the polynucleotide described above; (6) a method of inducing an immune response in an individual comprising the administration of the composition of (5) to induce an immune response; (7) an isolated polypeptide comprising any of the amino acid sequences as encoded by the polynucleotide described above; (8) a composition comprising a carrier and the polypeptide of (7); (9) a method of detecting *P. falciparum* in biological samples comprising contacting a biological sample with the isolated polynucleotide and detecting the hybridisation of the isolated polynucleotides with nucleic acids contained in the sample; (10) a method for eliciting an immune response in an individual comprising the administration of a composition comprising the polypeptides of (7) to an individual to induce an immune response in the individual; (11) an antibody that specifically binds to the *P. falciparum* polypeptide of (7); and (12) detecting *P. falciparum* antigens comprising contacting a sample from a subject with the polypeptide of (7) and detecting the presence of an antigen-antibody complex or detecting the stimulation of T-cells in the sample. The *P. falciparum* antigens and immunogenic peptides have cytostatic, anti-HIV, virucide, hepatotropic and antibacterial activities, and can be used in vaccines. The methods and compositions of the present invention are useful for inducing an immune response for the prevention and/or treatment of cancer and infectious diseases, such as AIDS, hepatitis, and bacterial infections. The present sequence represents a *P. falciparum* antigen amino acid sequence, which is used in the exemplification of the present invention.

XX Sequence 1781 AA;

Query Match Score 10.3%; DB 8; Length 1781;
Best Local Similarity 23.0%; Pred. No. 9.4;
Matches 44; Conservative 37; Mismatches 58; Indels 52; Gaps 8;
CC

Qy 20 VNGTQNIIILSLTFNKNQOTSYKDIENKVSKVLYFNRGISDIDILRS--KOAKYTVHFK 76

Db 946 INDDNNINMDNLNFTYNEQNN--NHEHNNKKWNVPNSNILLEKNEKTKNNYKIHOR 1003

Qy 77 -NGTFRVVDLKGATHADLINTSDIKAIISVNVDPKQVKDKEARANQVQPYTITVNGTQS 135

Db 1004 QNINQKNSDNENNINQKNTISKDKFQKINSYIDRK-----1038

Qy 136 NILSNLTFKKNQOISYKDIENKVSKVLYFNRGISDIDILRS--SNRGI--TDVDRLRLSKQAKFTV 183

Db 1039 -----LNTHKNNYKSYNNMEHNICVNQESSINNNNNNNLYTTDXDLRNNT--RTI 1090

Qy 184 NFKNQNTSKKVID 194;

Db 1091 NP-NDTKNNIIN 1100

Search completed: March 16, 2005, 10:42:35
Job time : 172 secs